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GTCGACCCACGCGTCCGCCACGCGTCCGGCCC	ATG GCG CCG CCC GCC CCG CTC GCC CTC GCG CTC	L L L L L L L	11
			66
S A A A L T L A A R P A A R L A L L	P G L G P G		31
TCC GCC GCG GCG CTC ACG CTG GCG GCG CCC GCG CCT AGC CCC GCG CTC GGC CCC GGA			126
P E C F T A N G A D Y R G T Q N W T A L			51
CCC GAG TGT TTC ACA GCC AAT GGT GCG GAT TAT AGG GGA ACA CAG AAC TGG ACA GCA CTA			186
Q G G K P C L F W N E T F Q H P Y N T L			71
CAA GCG GGG AAG CCA TGT CTG TTT TGG AAC GAG ACT TTC CAG CAT CCA TAC AAC ACT CTG			246
K Y P N G E G L G E H N Y C R N P D G			91
AAA TAC CCC AAC GGG GAG GGG GCG CTG GGT GAG CAC AAC TAT TGC AGA AAT CCA GAT GGA			306
D V S P W C Y V A E H E D G V Y W K Y C			111
GAC GTG AGC CCC TGG TGC TAT GTG GCA GAG CAC GAG GAT GGT GTC TAC TGG AAG TAC TGT			366
E I P A C Q M P G N L G C Y K D H G N P			131
GAG ATA CCT GCT TGC CAG ATG CCT GGA AAC CTT GGC TGC TAC AAG GAT CAT GGA AAC CCA			426
P P L T G T S K T S N K L T I Q T C I S			151
CCT CCT CTA ACT GGC ACC AGT AAA ACG TCC AAC AAA CTC ACC ATA CAA ACT TGC ATC AGT			486
F C R S Q R F K F A G M E S G Y A C F C			171
TTT TGT CGG AGT CAG AGG TTC AAG TTT GCT GGG ATG GAG TCA GGC TAT GCT TGC TTC TGT			546

Fig. 1A



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G	N	N	P	D	Y	W	K	Y	G	E	A	A	S	T	E	C	N	S	V	191
GGA	AAC	AAT	CCT	GAT	TAC	TGG	AAG	TAC	GGG	GAG	GCA	GCC	AGT	ACC	GAA	TGC	AAC	AGC	GTC	606
C	F	G	D	H	T	Q	P	C	G	G	D	G	R	I	I	L	F	D	T	211
TGC	TTC	GGG	GAT	CAC	ACC	CAA	CCC	TGT	GGT	GGC	GAT	GGC	AGG	ATC	ATC	CTC	TTT	GAT	ACT	666
L	V	G	A	C	G	G	N	Y	S	A	M	S	S	V	V	Y	S	P	D	231
CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	GCC	ATG	TCT	TCT	GTG	GTC	TAT	TCC	CCT	GAC	726
F	P	D	T	Y	A	T	G	R	V	C	Y	W	T	I	R	V	P	G	A	251
TTC	CCC	GAC	ACC	TAT	GCC	ACG	GGG	AGG	GTC	TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCG	GGG	GCC	786
S	H	I	H	F	S	F	P	L	F	D	I	R	D	S	A	D	M	V	E	271
TCC	CAC	ATC	CAC	TTC	AGC	TTC	CCC	CTA	TTT	GAC	ATC	AGG	GAC	TCG	GCG	GAC	ATG	GTG	GAG	846
L	L	D	G	Y	T	H	R	V	L	A	R	F	H	G	R	S	R	P	P	291
CTT	CTG	GAT	GGC	TAC	ACC	CAC	CGT	GTC	CTA	GCC	CGC	TTC	CAC	GGG	AGG	AGC	CGC	CCA	CCT	906
L	S	F	N	V	S	L	D	F	V	I	L	Y	F	F	S	D	R	I	N	311
CTG	TCC	TTC	AAC	GTC	TCT	CTG	GAC	TTC	GTC	ATC	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	966
Q	A	Q	G	F	A	V	L	Y	Q	A	V	K	E	E	L	P	Q	E	R	331
CAG	GCC	CAG	GGA	TTT	GCT	GTT	TTA	TAC	CAA	GCC	GTC	AAG	GAA	GAA	CTG	CCA	CAG	GAG	AGG	1026

Fig. 1B

P A V N Q T V A E V I T E Q A N L S V S	351
CCC GCT GTC AAC CAG ACG GTG GCC GAG GTG ATC ACG GAG CAG GCC AAC CTC AGT GTC AGC	1086
A A R S S K V L Y V I T T S P S H P P Q	371
GCT GCC CGG TCC TCC AAA GTC CTC TAT GTC ATC ACC ACC AGC CCC AGC CAC CCA CCT CAG	1146
T V P G S N S W A P P M G A G S H R V E	391
ACT GTC CCA GGT AGC AAT TCC TGG GCG CCA CCC ATG GGG GCT GGA AGC CAC AGA GTT GAA	1206
G W T V Y G L A T L L I L T V A I V A	411
GGA TGG ACA GTC TAT GGT CTG GCA ACT CTC CTC ATC ACA GTC ACA GCC ATT GTA GCA	1266
K I L L H V T F K S H R V P A S G D L R	431
AAG ATA CTT CTG CAC GTC ACA TTC AAA TCC CAT CGT GTT CCT CCT GCT TCA GGG GAC CTT AGG	1326
D C H Q P G T S G E I W S I F Y K P S T	451
GAT TGT CAT CAA CCA GGG ACT TCG GGG GAA ATC TGG AGC ATT TTT TAC AAG CCT TCC ACT	1386
S I S I I F K K K L K G Q S Q Q D D R N P	471
TCA ATT TCC ATC TTT AAG AAG AAA CTC AAG GGT CAG AGT CAA CAA GAT GAC CGC AAT CCC	1446
L V S D *	476
CTT GTG AGT GAC TAA	1461

Fig. 1C



AAACCCACTGTGCCTAGGACTTGAGGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGGTTCTTCTC 1540
TGACAGACTCTTCCCTCTCCTCTCCCTCTGCTCGGCTCTTCCGGGAAACCTCCTCCTACAGACTAGGAAGAGGCACCT 1620
GCTGCCAGGGCAGGCAGAGCCTGGATTCTCCTCCTGCTT 1657

Fig. 1D

GTCGACCCACGGTCCGCCCGGCTCCCGGTGCTGCCCTCTGCCCCGGCGCGCGGGGTCCCGCACTGACGGCC 79

M A P A P A A R L A L L S A A A L T L A 19
C ATG GCG CCG CCC GCC GCC CGT CTC GCG CTG CTC TCC GCC GCT GCG CTC ACT CTG GCG 137

A R P A P A P G P R S G P E C F T A N G A D 39
GCC CGG CCC GCG CCC GGT CCC CGC TCC GGC CCC GAG TGC TTC ACA GCC AAC AAC GGT GCA GAT 197

Y R G T Q S W T A L Q G G K P C L F W N 59
TAC AGG GGA ACA CAG AGC TGG ACA GCG CTG CAA GGT GGG AAG CCA TGT CTG TTC TGG AAC 257

E T F Q H P Y N T L K Y P N G E G L G 79
GAG ACT TTC CAG CAT CCG TAC AAC ACG CTG AAG TAC CCC AAC GGG GAA GGA GGA CTG GGC 317

E H N Y C R N P D G D V S P W C Y V A E 99
GAG CAC AAT TAT TGC AGA AAT CCA GAT GGA GAC GTG AGC CCT TGG TGC TAC GTG GCC GAG 377

Fig. 1E



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H	E	D	G	G	V	Y	W	K	Y	C	E	I	P	A	C	Q	M	P	G	N	119
CAT	GAG	GAC	GGA	GTC	TAC	TGG	AAG	TAC	TGT	GAA	ATT	CCT	GCC	TGC	CAG	ATG	CCT	GGA	AAC	437	
L	G	C	Y	K	D	H	G	N	P	P	P	P	L	T	G	T	S	K	T	S	139
CTT	GGC	TGC	TAC	AAG	GAT	CAT	GGA	AAC	CCA	CCT	CCT	CTC	ACG	GGC	ACC	AGT	AAA	ACC	TCT	497	
N	K	L	T	I	Q	T	C	I	S	F	C	R	S	Q	R	A	F	K	F	A	159
AAC	AAG	CTC	ACC	ATA	CAA	ACC	TGT	ATC	AGC	TTC	TGT	CGG	AGT	CAG	AGA	TTC	AAG	TTT	GCT	557	
G	M	E	S	G	Y	A	C	F	C	G	N	N	P	D	Y	W	K	H	G	179	
GGG	ATG	GAG	TCA	GGC	TAT	GCC	TGC	TTC	TGT	GGG	AAC	AAT	CCT	GAC	TAC	TGG	AAG	CAC	GGG	617	
E	A	A	S	T	E	C	N	S	V	C	F	G	D	H	T	Q	P	C	G	199	
GAG	GCG	GCC	AGC	ACC	GAG	TGC	AAT	AGT	GTC	TGC	TTC	GGG	GAC	CAC	ACG	CAG	CCC	TGC	GGT	677	
G	D	G	R	I	I	L	F	D	T	L	V	G	A	C	G	G	N	Y	S	219	
GGG	GAC	GGC	AGG	ATT	ATC	CTC	TTT	GAC	ACT	CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	737	
A	M	A	A	V	V	Y	S	P	D	F	P	D	T	Y	A	T	G	R	V	239	
GCC	ATG	GCA	GCC	GTG	GTG	TAC	TCC	CCT	GAC	TTC	CCT	GAC	ACC	TAC	GCC	ACT	GGC	AGA	GTC	797	
C	Y	W	T	I	R	V	P	G	A	S	R	I	H	F	N	F	T	L	F	259	
TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCA	GGA	GCC	TCT	CGC	ATC	CAT	TTC	AAC	TTC	ACC	CTG	TTT	857	
D	I	R	D	S	A	D	M	V	E	L	L	D	G	Y	T	H	R	V	L	279	
GAT	ATC	AGG	GAC	TCT	GCA	GAC	ATG	GTG	GAG	CTG	CTG	GAC	GGC	TAC	ACC	CAC	CGC	GTC	CTG	917	

Fig.1F



V R L S G R S R S R P P L S F N V S L D F V 299
GTC CGG CTC AGT GGG AGG AGC CGC CCT CTG TCT TTC AAT GTC TCT CTG GAT TTT GTC 977

I L Y F F S D R I N Q A Q G F A V L Y Q 319
ATT TTG TAT TTC TCT TCT GAT CGC ATC AAT CAG GCC CAG GGA TTT GCT GTG TTG TAC CAA 1037

A T K E E P P Q E R P A V N Q T L A E V 339
GCC ACC AAG GAG GAA CCG CCA CAG GAG AGA CCT GCT GTC AAC CAG ACC CTG GCA GAG GTG 1097

I T E Q A N L S V S A A H S S K V L Y V 359
ATC ACC GAG CAA GCC AAC CTC AGT GTC AGC GCT GCC CAC TCC TCC AAA GTC CTC TAT GTC 1157

I T P S P S H P P Q T A Q V A I P G H R 379
ATC ACC CCC AGC CCC AGC CAC CCT CCG CAG ACT GCC CAG GTA GCC ATT CCT GGG CAC CGT 1217

Q L G P T A T E W K D G L C T A W R P S 399
CAG TTG GGG CCA ACA GCC ACA GAG TGG AAG GAT GGA CTG TGT ACG GCC TGG CGA CCC TCC 1277

S S S Q S Q Q L S Q R F F C M S H L N L 419
TCA TCC TCA CAG TCA CAG CAG TTG TCG CAA AGA TTC TTC TGC ATG TCA CAT TTA AAT CTC 1337

I E S L H Q E T L G T V V S L G L L E I 439
ATC GAG TCC CTG CAT CAG GAG ACC TTA GGG ACT GTC GTC AGC CTG GGG CTT CTG GAG ATA 1397

S G P F S M N L P L Q S P S L R R S S R 459
TCT GGA CCA TTT TCT ATG AAC CTT CCA CTA CAA TCT CCA TCT TTA AGA AGC TCA AGG 1457

Fig.1G



V R V N K M T A I P S *

GTC AGA GTC AAC AAG ATG ACC GCA ATC CCC TCG TGA

471

1493

GTGACTGAAGCCCCACGCTGTCATGAGAGGCTCCGCTCCAAGCTCGAGTTTGCTCCCCCTGAGTTCTCCTCTGATGAGTTC 1572
CCTGCCCTTCCCATTCACACCATCTCTTTGGAGCACCCCTGCTTTAGAGGCAGCCAGCCCTGGGATCCTCCATCACAT 1651
GTACCAGCCTGGCTGCTGCTGGGATGGTAAGACAGGCCAGGCTGACAGGACACAGCTGGACCTGACTCCAGAAGA 1730
CTCTTGGGTGGGAGGTATAGTGTAGGATGAGTTTCTTGTCTCTCTCTGTTTGTCCACATACAGATCGGTTTC 1809
CCCTGTCTTTACAGTTTGCAATAGAGCCAGACTGAAAGAACTGTCAGGTTTCTAGGCTGGCCTGGTTCCCCACTAAGA 1888
GTGGCATTTGGCGCCCTAGAGGCCCAAGGCCAGTGTAGGCTTGGAGCTTCTCTGCTGCCAACTACCATGTGTCACT 1967
AGTCCGAGGGGACTGAGAGCAGGGCCACACACAGATGTCATCTTTCTAGAGGTTCTTTTAGTACCCACTGACCAATGG 2046
GGCAAGCCTGAGGATTGGTCCATCTGTTTGTCCATGGAACAGACACAGTGAACCTTCTGGATACCTAGACTTAAGTACC 2125
TAGCCCTCAAGTAGTTGCCAATCCTGTGGAATCAGAATTCAGCCTGTCTTCTGTCTCAGCCCCAAGCCTGTAGCCTAG 2204
AGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCACAGAGCTGGGCTGTAGCCTAGAGC 2283
TGGGCTGTAGCAÇAGAGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCACAGAGCTGGGCTGTAGCACAGAGCTGG 2362
GGCTGTAGCCTAGAGCTGGGCTGTAGCACAGAGCTGGGCTGTAACTCAGCGATCAAGAGCTTGCTTTGTATACATCG 2441
GACCCTAGGTTCTATCCCAGCACTATCAGAAAGGTGGGAGAGAAAGACTGCACCATAGCATGCGGCAGCATCTGTGG 2520
TTCCCTACGTGAGGTGTCATCATTTTAAAGCAGATCAAACTACCGCGAGTTTGTCTCTTGTCTCTTATCATGGGAGC 2599
AGAGTAGGAGTAAGGGCTCTGGTCTTGTCTCATTTGTCCCCCAGACAGGGAGGCAAGAAAGTCAAGCTTGGGAAC 2678
GATCCTCCAGGAAAGCTGCAAGATTGAGAGACCCAGCTGCAGTTGGAGAGGAGGCGCATCCCCGACTGAGAAATC 2757
CTGCAGTCTGGAAGTGGCCTTTGTGACGACGAGCTGTGCCCTGAAGGTAGACCTTGGTCACTCTCTGCCAGCCCTGA 2836
GCCTCTGCTCTCCTGGGTACCCCTCCTGGAACACCATGTCTAACCTTCCCCGAGTCTCTCAGTCACTGCCATTGAGGCC 2915
TCCTCTAGCTGCTCCCCAGGACTGTCTGGGCCATCTGGGATCAGGGAGAGGAGGAGTCACTGACGAGGCAG 2994
TGACCTGAGCTGATGAGTCAACAGAGGACACAGAGTCTACAGTGGGCTGGCTGGCTCAGCTCCTATGGGAGGCC 3073
TACAGGGGTACTAAGCTAGGGGTCTATCTCATTTGATCTGGGAAAGGCTACAGGCTCCTGGATGTGAAGACAGGCC 3152
CACTACATAAGAAGACCCTGGAAATAGACTGACAGGAGCAGGTTCCACTCTAGGCTGTCCATAGCGTTTGCAGGACTC 3231

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Fig.1H



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CCCTGAGACCAAGTGTGAGTCACAGAGTGCCATGTGCGTAGTGCTAATAAGGATATGGGTTCTTAACCAGGGAAGGCTC 3310
ATAGCAGGCCAGGACATTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACTCACCTGTCTCTTCCT 3389
ATCTCGGACACAGGAAGCAAGCCCCAGTGTGGTGCCAGCTGCGGCTCAGCATTTGGTGTCCCCAGGAAGGCGGTGGATG 3468
TGCCCCACGCTCCTTTTGCTGTGGGCTGGCACAGCCCCAACACTGCAGGGCCCCACCTTCTCTTTGGGGGTAGGGACAC 3547
ATAAGGAAACATAACCCACCTCCAACAACAGCAGAGGACAGTGGGAAGGAGGCTGTAAATCACCCAGGCCAGACCTC 3626
CAGAAATGACAGGCACAGTCTGTTAGAACCTGTAGGCAGCCAGTCACAGAGGGCCTTTGTGCTGGTAACACCCTGCCCTG 3705
GAGCATAGGGGTAAGCCGAGGAGAGAGCAGCCCTCAGAGACATCAGCTAAAACATAGGTGCCCTATGTCCCTCCCT 3784
TCCTGTCACTGCTTACAAAGCAGAGACAGAGTAGGAAAGAGTCTTCATCCTCTCCACATCAGCAAGGATAGGGCT 3863
GCGGCTGCCATAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGCTCTGGCTTCAGACTCCTCAGCCA 3942
AAAGCTCTTGAAGATCAAAAGCTCTGGCGGGTACAGCTGTCTGGCCTGTGGCCAGCCCATGGGATGTGCTGGCCAG 4021
GTGCCACCCACGGCTCACTGTCAATCCAGGAGGACCCACCTGATGCTCCTCATCATCCGCTGGCCTGACACTATCA 4100
GAGCTCGCGCCGGCTGTTGCCAGGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGATGGCCTCCAGA 4179
CTCTGTACGCTCTGCAGGGCCACACAAGTCTCCGAGCCAAAGTCCACAAGCCTCCATGGTTCCCTGGCTCCTCCT 4258
GTGGAGTGTCTGATGTCTGAGGTCTGCTTTGGGTACCGCCCTGGGAACTGCTAACCTCCGATTTGGTCCCTTTGT 4337
GTCCTGTTTACTGCTCCTTCTACCTCCAGGTCACTTAGCTCTGGCTGCTCTGGCTGGGAGTGGGGGTGGGATGCT 4416
GGCTGACCCCCACCTGCTGCCAACAGAACCTGGGGCTCACACGGGCTCCTGTCTTGCCAAAGCTGGAGCTGAGC 4495
ACACTGGCCAGGCTGAGTGGGCAGAGCAACAAGTGGAAAGGGATCTCTCCTTAGAGGGAGGTGGCCGAAGGTGT 4574
AGATCCAGCGAGGAGCTGCCATCCCCGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAACTCTCACCCCTCCAGCAG 4653
GGATATGACTTTGGACAACAAGGCTTTATTTGTAATAATGCTCTTAATATGCAACTTTGAGAAATAAGATAAGAAACATCA 4732
TGTATTTTAAATAATAAATGAAGTGTGACACACTGTATACAATTTAATATATAATTTTAGGATTTTGTATTAAAGAA 4811
AATGGAATGTGATGGTAACTTTTACAAAAGAGAGAAAATGTTATTTTACTGTTTGAAGAAAATAAATATTCTCA 4890
TTGTTGTAGAAAAAATAAATAAAGGCGGCGCCG 4928

Fig.11



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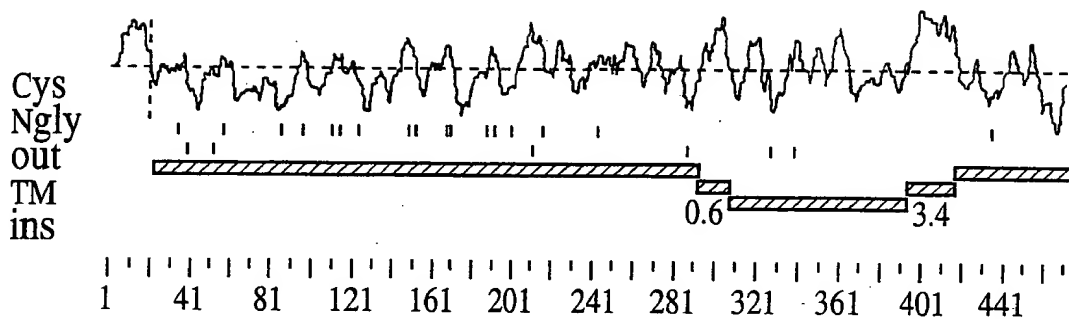


Fig. 1L

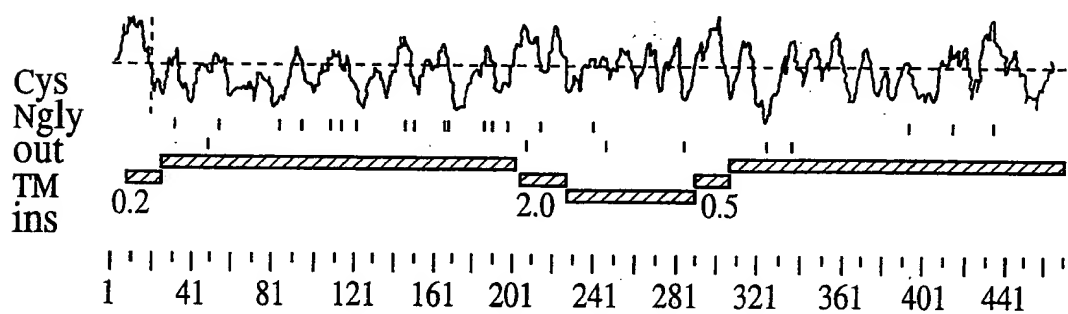


Fig. 1M



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GCGGCCGCTCGGATCTAGAACTAGTA	ATG	ATG	CTG	CCT	CAA	AAC	TCG	TGG	CAT	ATT	GAT	TTT	GGA	13
														66
R C C C H Q N L F S A V V T C I L L L N														33
AGA TGC TGC TGT CAT CAG AAC CTT TTC TCT GCT GTG GTA ACT TGC ATC CTG CTC CTG AAT														126
S C C F L I S S F N G T D L E L R L V N G														53
TCC TGC TTT CTC ATC AGC AGT TTT AAT GGA ACA GAT TTG GAG TTG AGG CTG GTC AAT GGA														186
D G P C C S G T V E V K F Q G Q W G T V C														73
GAC GGT CCC TGC TCT GGG ACA GTG GAG GTG AAA TTC CAG GGA CAG TGG GGG ACT GTG TGT														246
D D G W N T A S T V V C K Q L G C P F														93
GAT GAT GGG TGG AAC ACT ACT GCC TCA ACT GTC GTG TGC AAA CAG CTT GGA TGT CCA TTT														306
S F A M F R F G Q A V T R H G K I W L D														113
TCT TTC GCC ATG TTT CGT TTT GGA CAA GCC GTG ACT AGA CAT GGA AAA ATT TGG CTT GAT														366
D V S C Y G N E S A L W E C Q H R E W G														133
GAT GTT TCC TGT TAT GGA AAT GAG TCA GCT CTC TGG GAA TGT CAA CAC CGG GAA TGG GGA														426
S H N C Y H G E D V G V N C Y G E A N L														153
AGC CAT AAC TGT TAT CAT GGA GAA GAT GTT GGT GTG AAC TGT TAT GGT GAA GCC AAT CTG														486

Fig. 2A

G	L	R	L	V	D	G	N	N	S	C	S	G	R	V	E	V	K	F	Q	173
GGT	TTG	AGG	CTA	GTG	GAT	GGA	AAC	AAC	TCC	TGT	TCA	GGG	AGA	GTG	GAG	GTG	AAA	TTC	CAA	546
E	R	W	G	T	I	C	D	D	G	W	N	L	N	T	A	A	V	V	C	193
GAA	AGG	TGG	GGG	ACT	ATA	TGT	GAT	GAT	GGG	TGG	AAC	TTG	AAT	ACT	GCT	GCC	GTG	GTG	TGC	606
R	Q	L	G	C	P	S	S	F	I	S	S	G	V	V	N	S	P	A	V	213
AGG	CAA	CTA	GGA	TGT	CCA	TCT	TCT	TTT	ATT	TCT	TCT	GGA	GTT	GTT	AAT	AGC	CCT	GCT	GTA	666
L	R	P	I	W	L	D	D	I	L	C	Q	G	N	E	L	A	L	W	N	233
TTG	CGC	CCC	ATT	TGG	CTG	GAT	GAC	ATT	TTA	TGC	CAG	GGG	AAT	GAG	TTG	GCA	CTC	TGG	AAT	726
C	R	H	R	G	W	G	N	H	D	C	S	H	N	E	D	V	T	L	T	253
TGC	AGA	CAT	CGT	GGA	TGG	GGA	AAT	CAT	GAC	TGC	AGT	CAC	AAT	GAG	GAT	GTC	ACA	TTA	ACT	786
C	Y	D	S	S	D	L	E	L	R	L	V	G	G	T	N	R	C	M	G	273
TGT	TAT	GAT	AGT	AGT	GAT	CTT	GAA	CTA	AGG	CTT	GTA	GGT	GGA	ACT	AAC	CGC	TGT	ATG	GGG	846
R	V	E	L	K	I	Q	G	R	W	G	T	V	C	H	H	K	W	N	N	293
AGA	GTA	GAG	CTG	AAA	ATC	CAA	GGA	AGG	TGG	GGG	ACC	GTA	TGC	CAC	CAT	AAG	TGG	AAC	AAT	906
A	A	A	D	V	V	C	K	Q	L	G	C	G	T	A	L	H	F	A	G	313
GCT	GCA	GCT	GAT	GTC	GTA	TGC	AAG	CAG	TTG	GGA	TGT	GGA	ACC	GCA	CTT	CAC	TTC	GCT	GGC	966
L	P	H	L	Q	S	G	S	D	V	V	W	L	D	G	V	S	C	S	G	333
TTG	CCT	CAT	TTG	CAG	TCA	GGG	TCT	GAT	GTT	GTA	TGG	CTT	GAT	GGT	GTC	TCC	TGC	TCC	GGT	1026

Fig. 2B

N	E	S	F	L	W	D	C	R	H	S	G	T	V	N	F	D	C	L	H	353
AAT	GAA	TCT	TTT	CTT	TGG	GAC	TGC	AGA	CAT	TCC	GGA	ACC	GTC	AAT	TTT	GAC	TGT	CTT	CAT	1086
Q	N	D	V	S	V	I	C	S	D	G	A	D	L	E	L	R	L	A	D	373
CAA	AAC	GAT	GTG	TCT	GTG	ATC	TGC	TCA	GAT	GGA	GCA	GAT	TTG	GAA	CTG	CGA	CTA	GCA	GAT	1146
G	S	N	N	C	S	G	R	V	E	V	R	I	H	E	Q	W	W	T	I	393
GGA	AGT	AAC	AAT	TGT	TCA	GGG	AGA	GTA	GAG	GTG	AGA	ATT	CAT	GAA	CAG	TGG	TGG	ACA	ATA	1206
C	D	Q	N	W	K	N	E	Q	A	L	V	V	C	K	Q	L	G	C	P	413
TGT	GAC	CAG	AAC	TGG	AAG	AAT	GAA	CAA	GCC	CTT	GTG	GTT	TGT	AAG	CAG	CTA	GGA	TGT	CCG	1266
F	S	V	F	G	S	R	R	A	K	P	S	N	E	A	R	D	I	W	I	433
TTC	AGC	GTC	TTT	GGC	AGT	CGT	CGT	GCT	AAA	CCT	AGT	AAT	GAA	GCT	AGA	GAC	ATT	TGG	ATA	1326
N	S	I	S	C	T	G	N	E	S	A	L	W	D	C	T	Y	D	G	K	453
AAC	AGC	ATA	TCT	TGC	ACT	GGG	AAT	GAG	TCA	GCT	CTC	TGG	GAC	TGC	ACA	TAT	GAT	GGA	AAA	1386
A	K	R	T	C	F	R	R	S	D	A	G	V	I	C	S	D	K	A	D	473
GCA	AAG	CGA	ACA	TGC	TTC	CGA	AGA	TCA	GAT	GCT	GGA	GTA	ATT	TGT	TCT	GAT	AAG	GCA	GAT	1446
L	D	L	R	L	V	G	A	H	S	P	C	Y	G	R	L	E	V	K	Y	493
CTG	GAC	CTA	AGG	CTT	GTC	GGG	GCT	CAT	AGC	CCC	TGT	TAT	GGG	AGA	TTG	GAG	GTG	AAA	TAC	1506
Q	G	E	W	G	T	V	C	H	D	R	W	S	T	R	N	A	A	V	V	513
CAA	GGA	GAG	TGG	GGG	ACT	GTG	TGT	CAT	GAC	AGA	TGG	AGC	ACA	AGG	AAT	GCA	GCT	GTT	GTG	1566

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Fig. 2C



C K Q L G C G K P M H V F G M T Y F K E 533
TGT AAA CAA TTG GGA TGT GGA AAG CCT ATG CAT GTG TTT GGT ATG ACC TAT TTT AAA GAA 1626

A S G P I W L D D V S C I G N E S N I W 553
GCA TCA GGA CCT ATT TGG CTG GAT GAC GTT TCT TGT TGC ATT GGA AAT GAG TCA AAT ATC TGG 1686

D C E H S G W G K H N C V H R E D V I V 573
GAC TGT GAA CAC AGT GGA TGG GGA AAG CAT AAT TGT GTA CAC AGA GAG GAT GTG ATT GTA 1746

T C S G D A T W G L R L V G G S N R C S 593
ACC TGC TCA GGT GAT GCA ACA TGG GGC CTG AGG CTG GTG GGC AGC AAC CGC TGC TCG 1806

G R L E V Y F Q G R W G T V C D D G W N 613
GGA AGA CTG GAG GTG TAC TTT CAA GGA CGG TGG TGG GGC ACA GTG TGT GAT GAC GGC TGG AAC 1866

S K A A A V V C S Q L D C P S S I I G M 633
AGT AAA GCT GCA GCT GTG GTG TGT AGC CAG CTG GAC TGC CCA TCT TCT ATC ATT GGC ATG 1926

G L G N A S T G Y G K I W L D D V S C D 653
GGT CTG GGA AAC GCT TCT ACA GGA TAT GGA AAA ATT TGG CTC GAT GAT GTT TCC TGT GAT 1986

G D E S D L W S C R N S G W G N N D C S 673
GGA GAT GAG TCA GAT CTC TGG TCA TGC AGG AAC AGT GGG TGG GGA AAT AAT GAC TGC AGT 2046

H S E D V G V I C S D A S D M E L R L V 693
CAC AGT GAA GAT GTT GGA GTG ATC TGT TCT GAT GCA TCG GAT ATG GAG CTG AGG CTT GTG 2106

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Fig. 2D



G G S S R C A G K V E V N V Q G A V G I 713
GGT GGA AGC AGC AGG TGT GCT GGA AAA GTT GAG GTG AAT GTC CAG GGT GCC GTG GGA ATT 2166

L C A N G G W G M N I A E V V C R Q L E C 733
CTG TGT GCT AAT GGC TGG GGA ATG AAC ATT GCT GAA GTT GTT TGC AGG CAA CTT GAA TGT 2226

G S A I R V S R E P H F T E R T L H I L 753
GGG TCT GCA ATC AGG GTC TCC AGA GAG CCT CAT TTC ACA GAA AGA ACA TTA CAC ATC TTA 2286

M S N S G C T G G E A S L W D C I R W E 773
ATG TCG AAT TCT GGC TGC ACT GGA GGG GAA GCC TCT CTC TGG GAT TGT ATA CGA TGG GAG 2346

W K Q T A C H L N M E A S L I C S A H R 793
TGG AAA CAG ACT GCG TGT CAT TTA AAT ATG GAA GCA AGT TTG ATC TGC TCA GCC CAC AGG 2406

Q P R L V G A D M P C S G R V E V K H A 813
CAG CCC AGG CTG GTT GGA GCT GAT ATG CCC TGC TCT TCT GGA CGT GTT GAA GTG AAA CAT GCA 2466

D T W R S V C D S D F S L S L H A A N V L C 833
GAC ACA TGG CGC TCT GTC TGT GAT TCT GAT TTC TCT TCT CTT CAT GCT GCC AAT GTG CTG TGC 2526

R E L N C G D A I S L S V G D H F G K G 853
AGA GAA TTA AAT TGT GGA GAT GCC ATA TCT CTT TCT GTG GGA GAT CAC TTT GGA AAA GGG 2586

N G L T W A E K F Q C E G S E T H L A L 873
AAT GGT CTA ACT TGG GCC GAA AAG TTC CAG TGT GAA GGG AGT GAA ACT CAC CTT GCA TTA 2646

Fig. 2E



17/95

C P I V Q H P E D T C I H S R E V G V V 893
TGC CCC ATT GTT CAA CAT CCG GAA GAC ACT TGT ATC CAC AGC AGA GAA GTT GGA GTT GTC 2706

C S R Y T D V R L V N G K S Q C D G Q V 913
TGT TCC CGA TAT ACA GAT GTC CGA CTT GTG AAT GGC AAA TCC CAG TGT GAC GGG CAA GTG 2766

E I N V L G H W G S L C D T H W D P E D 933
GAG ATC AAC GTG CTT GGA CAC TGG GGC TCA CTG TGT GAC ACC CAC TGG GAC CCA GAA GAT 2826

A R V L C R Q L S C G T A L S T T G G K 953
GCC CGT GTT CTA TGC AGA CAG CTC AGC TGT GGG ACT GCT CTC TCA ACC ACA GGA GGA AAA 2886

Y I G E R S V R V W G H R F H C L G N E 973
TAT ATT GGA GAA AGA AGT GTT CGT GTG TGG GGA CAC AGG TTT CAT TGC TTA TTA GGG AAT GAG 2946

S L L D N C Q M T V L G A P P C I H G N 993
TCA CTT CTG GAT AAC TGT CAA ATG ACA GGT CTT GGA GCA CCT CCC TGT ATC CAT GGA AAT 3006

T V S V I C T G S L T Q P L F P C L A N 1013
ACT GTC TCT GTG ATC TGC ACA GGA AGC CTG ACC CAG CCA CTG TTT CCA TGC CTC GCA AAT 3066

V S D P Y L S A V P E G S A L I C L E D 1033
GTA TCT GAC CCA TAT TTG TCT GCA GTT CCA GAG GGC AGT GCT TTG ATC TGC TTA GAG GAC 3126

K R L R L V D G D S R C A G R V E I Y H 1053
AAA CGG CTC CGC CTA GTG GAT GGG GAC AGC CGC TGT GCC GGG AGA GTA GAG ATC TAT CAC 3186

Fig. 2F

D	G	F	W	G	T	I	C	D	D	G	W	D	L	S	D	A	H	V	V	1073
GAC	GGC	TTC	TGG	GGC	ACC	ATC	TGT	GAT	GAC	GAC	TGG	GAC	CTG	AGC	GAT	GCC	CAC	GTG	GTG	3246
C	Q	K	L	G	C	G	V	A	F	N	A	T	V	S	A	H	F	G	E	1093
TGT	CAA	AAG	CTG	GGC	TGT	GGA	GTG	GCC	TTC	AAT	GCC	ACG	GTC	TCT	GCT	CAC	TTT	GGG	GAG	3306
G	S	G	P	I	W	L	D	D	L	N	C	T	G	T	E	S	H	L	W	1113
GGG	TCA	GGG	CCC	ATC	TGG	CTG	GAT	GAC	CTG	AAC	TGC	ACA	GGA	ACG	GAG	TCC	CAC	TTG	TGG	3366
Q	C	P	S	R	G	W	G	Q	H	D	C	R	H	K	E	D	A	G	V	1133
CAG	TGC	CCT	TCC	CGC	GGC	TGG	GGG	CAG	CAC	GAC	TGC	AGG	CAC	AAG	GAG	GAC	GCA	GGG	GTC	3426
I	C	S	E	F	T	A	L	R	L	Y	S	E	T	E	T	E	S	C	A	1153
ATC	TGC	TCA	GAA	TTC	ACA	GCC	TTG	AGG	CTC	TAC	AGT	GAA	ACT	GAA	ACA	GAG	AGC	TGT	GCT	3486
G	R	L	E	V	F	Y	N	G	T	W	G	S	V	G	R	R	N	I	T	1173
GGG	AGA	TTG	GAA	GTC	TTC	TAT	AAC	GGG	ACC	TGG	GGC	AGC	GTC	GGC	AGG	AGG	AAC	ATC	ACC	3546
T	A	I	A	G	I	V	C	R	Q	L	G	C	G	E	N	G	V	V	S	1193
ACA	GCC	ATA	GCA	GGC	ATT	GTG	TGC	AGG	CAG	CTG	GGC	TGT	GGG	GAG	AAT	GGA	GTT	GTC	AGC	3606
L	A	P	L	S	K	T	G	S	G	F	M	W	V	D	D	I	Q	C	P	1213
CTC	GCC	CCT	TTA	TCT	AAG	ACA	GGC	TCT	GGT	TTC	ATG	TGG	GTG	GAT	GAC	ATT	CAG	TGT	CCT	3666
K	T	H	I	S	I	W	Q	C	L	S	A	P	W	E	R	R	I	S	S	1233
AAA	ACG	CAT	ATC	TCC	ATA	TGG	CAG	TGC	CTG	TCT	GCC	CCA	TGG	GAG	CGA	AGA	ATC	TCC	AGC	3726

Fig. 2G

P	A	E	E	T	W	I	T	C	E	D	R	I	R	V	R	G	G	D	T	1253
CCA	GCA	GAA	GAG	ACC	TGG	ATC	ACA	TGT	GAA	GAT	AGA	ATA	AGA	GTG	CGT	GGA	GGA	GAC	ACC	3786
E	C	S	G	R	V	E	I	W	H	A	G	S	W	G	T	V	C	D	D	1273
GAG	TGC	TCT	GGG	AGA	GTG	GAG	ATC	TGG	CAC	GCA	GGC	TCC	TGG	GGC	ACA	GTG	TGT	GAT	GAC	3846
S	W	D	L	A	E	A	E	V	V	C	Q	Q	L	G	C	G	S	A	L	1293
TCC	TGG	GAC	CTG	GCC	GAG	GCG	GAA	GTG	GTG	TGT	CAG	CAG	CTG	GGC	TGT	GGC	TCT	GCT	CTG	3906
A	A	L	R	D	A	S	F	G	Q	G	T	G	T	I	W	L	D	D	M	1313
GCT	GCC	CTG	AGG	GAC	GCT	TCG	TTT	GGC	CAG	GGA	ACT	GGA	ACC	ATC	TGG	TTG	GAT	GAC	ATG	3966
R	C	K	G	N	E	S	F	L	W	D	C	H	A	K	P	W	G	Q	S	1333
CGG	TGC	AAA	GGA	AAT	GAG	TCA	TTT	CTA	TGG	GAC	TGT	CAC	GCC	AAA	CCC	TGG	GGA	CAG	AGT	4026
D	C	G	H	K	E	D	A	G	V	R	C	S	G	Q	S	L	K	S	L	1353
GAC	TGT	GGA	CAC	AAG	GAA	GAT	GCT	GGC	GTG	AGG	TGC	TCT	GGA	CAG	TCG	CTG	AAA	TCA	CTG	4086
N	A	S	S	G	H	L	A	L	I	L	S	S	I	F	G	L	L	L	L	1373
AAT	GCC	TCC	TCA	GGT	CAT	TTA	GCA	CTT	ATT	TTA	TCC	AGT	ATC	TTT	GGG	CTC	CTT	CTC	CTG	4146
V	L	F	I	L	F	L	T	W	C	R	V	Q	K	Q	K	H	L	P	L	1393
GTT	CTG	TTT	ATT	CTA	TTT	CTC	ACG	TGG	TGC	CGA	GTT	CAG	AAA	CAA	AAA	CAT	CTG	CCC	CTC	4206
R	V	S	T	R	R	R	G	S	L	E	E	N	L	F	H	E	M	E	T	1413
AGA	GTT	TCA	ACC	AGA	AGG	AGG	GGT	TCT	CTC	GAG	GAG	AAT	TTA	TTC	CAT	GAG	ATG	GAG	ACC	4266



C L K R E D P H G T S D D T P N H G 1433
TGC CTC AAG AGA GAG GAC CCA CAT GGG ACA AGA ACC TCA GAT GAC ACC CCC AAC CAT GGT 4326

C E D A S D D T S L L L G V L P A S E A T K 1453
TGT GAA GAT GCT AGC GAC ACA TCG CTG TTG GGA GTT CTT CCT GCC TCT GAA GCC ACA AAA 4386

*

TGA

1454
4389

CTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAGGAGACAACTTTTAAATGAATAAGAGGA 4468
AGTCAAGTTGCCCTATGGAAAACCTTGTCCAAATAACATTTCTTGAACAATAGGAGAACACAGCTAAATTGATAAAAGACTGG 4547
TGATAATAAAAATTGAATTATGTATATCACTGTTAAAAAAAACAAAAACAAAAACGACCGTGGGTCG 4626
AC 4628

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Fig. 2I

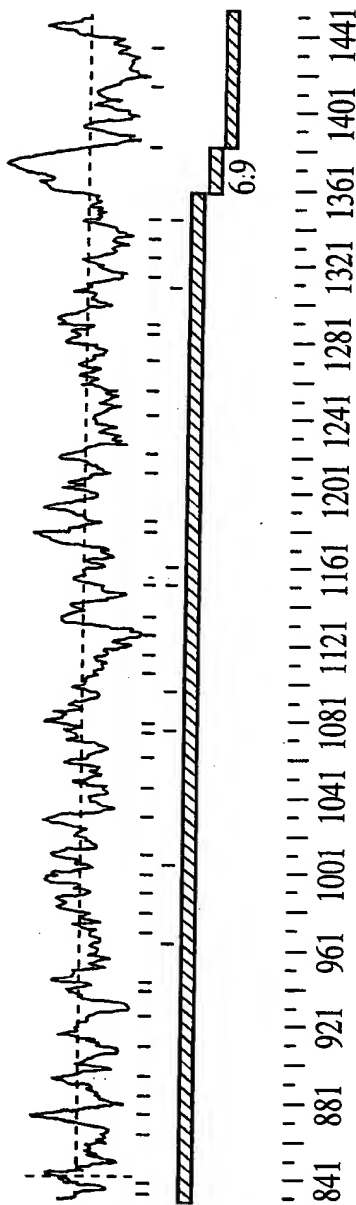
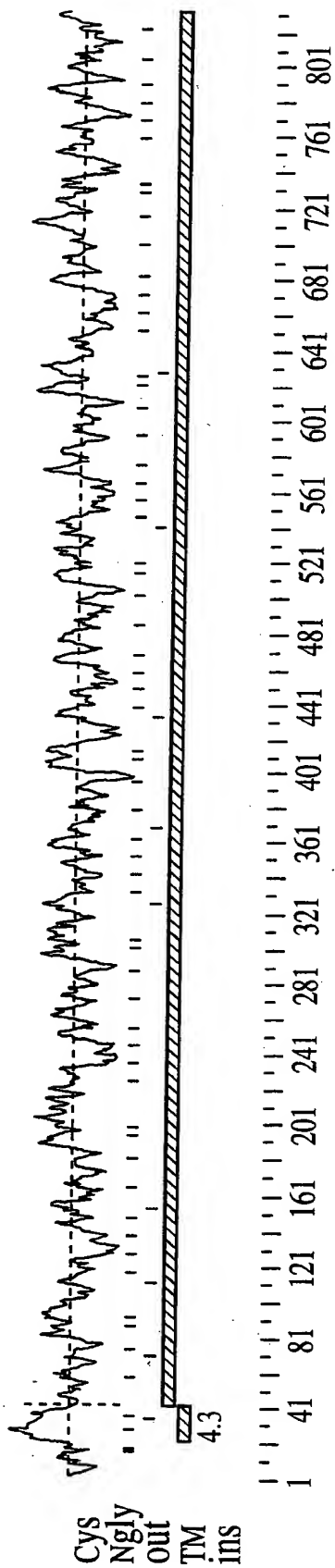


Fig. 2J

Hum.	MMLPQNSWHIDFGRCCCHQNLFSVVT	CILLNSCFLISSFNGTDL	LELRLVNGDGPCSGTVEVKFQGWG	70
WC1	MAL-----GR---HLSLRGL---	CVLLLT--MVG---	GQALELRLKDGVHRCEGRVEVKHQGEWG	50
	10	20	30	40
Hum.	TVCDDGWNTTASTVVCKQLGCPFSFAMERFGQAVTR-HGKIWLDDV	SCYGNESALWECQH---	REWGSHN	130
WC1	TVDGYRWTLKDASVVCRLGCCGAAIG-FPGGAYFGPGLGPIWLLYT	SCGTESTVSDCEHSNIKDYRNDG		110
	60	70	80	90
Hum.	CYHGEDVGVNCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWN	LNTAAVVCRLGCPSSFISSG		200
WC1	YNHGRDAGVVCSG-----FVRLAGGDGPCSGRVEVHSGEAWIPVSDGNFT	LATAQIICAELGCGKAVSVLG		180
	120	130	140	150
Hum.	VVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVT	LTCDSSDLELRLVGTNRCMGRVE		270
WC1	HELFRESSAQVWAEFFRCEGEEPELWVCPRPVCPGGTCHHSGSAQVVC	SAYSEVRL-MTNGSSQCEGQVE		250
	190	200	210	220

Fig. 2K



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Hum. LKIQRWGTVCHHKWNNAADVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSNESFLWDCRHS GT 280 290 300 310 320 330 340
WC1 MNISQWRALCASHWSLANANVICRQLGCGVAISTPGPHLVEEGDQILTARFHCSCGAESFLWSCPV TAL 260 270 280 290 300 310 320
Hum. VNFDC LHQNDVSICSDGADLELR LADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSV 350 360 370 380 390 400 410
WC1 GGPDCSHGNTASVICS-GNQI-----QVLPQCND-----SV 330 340 350
Hum. FGSRRRAKPSNEARDIWINISICTGNESALWDCTYDGKAKRTCFRRSDAGVICSDKADLDLRLVGAHSPCY 420 430 440 450 460 470 480
WC1 -----SQPTGSA-----ASEDSA-----PY-----CSDSRQL--RLVDGGGGPCA 360 370 380
Hum. GRLEVKYQGEWGTVCHDRWSTRNAAVVCCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE 490 500 510 520 530 540 550
WC1 GRVEILDQGSWGTICDDGWDLDARVVCRCQLGCGEALNATGSAHFGAGSGPIWLDNLNCTGKESHVWRCP 390 400 410 420 430 440 450

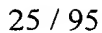
Fig. 2L



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Hum. HSGWGKHNCHREDVIVTCSGDATWGLRLVGGNRCGRLEVFQGRWGTVCDDGWNASKAAAVVCSQLDC
460 470 480 490 500 510 520
WC1 SRGWGQHNCRHKQDAGVICS--EFLALRMVSEDQQCAGWLEVFYNGTWGVCVRNPMEDITVSTICRQLGC
460 470 480 490 500 510 520
Hum. PSSIGMGLGNASTGYGKIWLDDVSCDGEDSLWSCRNSGWNDCSHSEVDGVICSDASDMELRLVGG
630 640 650 660 670 680 690
WC1 GDSGTLNSSVALREGFRPQWVDRIQCRKTDTSWQCPSPDPWYNNSCSPKEEAYIWCADSR--QIRLVDGG
530 540 550 560 570 580 590
Hum. SRCAGKVEVNVQGA VGILCANGWMNIAEVVCRQLECGSAIRVSREPHTERTLHILMSNSGCTGGEASL
700 710 720 730 740 750 760
WC1 GRCSGRVEILDQGSWGTICDDRWDLDARVVCKQLGCGEALDATVSSFFGTGSGPIWLDEVNCRGEESQV
600 610 620 630 640 650 660
Hum. WDCIRWEWKQTACHLNMEASLICS AHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCREL
770 780 790 800 810 820 830
WC1 WRCPSWGRQHNCNHQEDAGVICS GF--VRLAGGDGPCSGRVEVHSGEAWTPVSDGNFTLPTAQVICAEL
670 680 690 700 710 720 730

Fig. 2M



	840	850	860	870	880	890	900
Hum.	NCGDAISLSVGDHFGKGNGLTWA	AKFQCEGSETHALCP	IVQHPED	TCIHSRE	VGVC	SR	YTDVRLV-NG
	:: ::::	:	:: ::::	:: ::::	:	:: ::::	:: ::::
WC1	GCGKAVSVLGHMPFRES	DGQVAAEFRC	DGGEPELW	SCPRVPC	GGTCLHSGAAQ	VVC	SVYTEVQLMKNG
	740	750	760	770	780	790	800

	910	920	930	940	950	960	970
Hum.	KSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTGGKYIGERSVRVWGH	RFHCLGNESL					

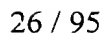
WC1	TSQCEGQVEMKISGRWRALCASHWSLANANVVCRLGCGVAISTPRGPHLVEGGDQISTAQFHCSGAESF						
	810	820	830	840	850	860	870

[illegible]

	1050	1060	1070	1080	1090	1100	1110					
Hum.	AGRVEIYH	DGFWGTIC	DDGWDLS	DAHVVCQ	KLGC	GVAFNAT	VS	AHFGEGSGPIW	LDL	DLNCTGT	ESH	WQC

WC1	GGRVEILD	QGSWGTIC	DDDDWD	LDLDDAR	VVCRQL	GCCEAL	NATG	SAHFGAGSGPI	WLDL	DLNCTG	KESH	VWRC
	950	960	970	980	990	1000	1010					

Fig. 2N



	1120	1130	1140	1150	1160	1170	1180
Hum.	PSRGWGQHDCRHKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGRNITTAIAGIVCRQLG						
	::::::::::::::::::::::::::	::::	::	::::::::::::::::::::::	::	::::::::::::	
WC1	PSRGWGRHDCRHKEDAGVICSEFTALRMVSEDQQ--CAGWLEVFYNGTWGSVCRSPMEDITVSVICRQLG						
	1020	1030	1040	1050	1060	1070	

```

1190      1200      1210      1220      1230      1240
Hum.  CGENG\SLAPLSKTGSGFMWDDIQCPKTHISIWQCLAPWERRISSPAEETWITCEDR-----
      :...: . . : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   CGDSGSLNTSVGLREGSRPRWVDLIQCRKMDTSLWQCPGPGWKYSSCPKEEAYISCEGRRPKSCPTAAA
1080      1090      1100      1110      1120      1130      1140

```

	1250	1260	1270	1280	1290	1300
Hum. -----	IRVRGGDTECSGRVEI	WHAGSWGTV	CDDSWDLAEAEVVCQ	QLGCGSALAA	LRDASF	GQGTGIW

WC1 CTDREKLR	GGDSECSGRVEV	WHNGSWGTV	CDDSWSLAEAEVVCQ	QLGCGQALEAVR	SAAF	PGNGSIW
1150	1160	1170	1180	1190	1200	1210

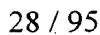
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1310      1320      1330      1340      1350      1360
Hum.  LDDMRCKNESFLWDCHAKPWGQSDCGHKEDAGVRCG-----QSLKSLNASSGHLALI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  LDEVQCGGRESSLWDCVAEPWGQSDCKHEEDAGVRCSGVRTTLPTTTAGTRTTSNLSLPGIFSLPGVLCI
1220      1230      1240      1250      1260      1270      1280

```

Fig. 20

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	80	90	100	110	120	130	140
Hum.	CTGTGGTAACTTGCATCCTGCTCCTGAATTCCTGCTTCTCATCAGCAGTTTAAATGGAACAGATTGGA						
	: : . . : : . . : : . . : : . . : : . . : : . . : : . . : : . . : : . . : : . .						
WC1	C-GGGGACTCT-GTGTCTCCTCCTCT-----CGGCA-----CATGGTGGTGGTCAAGCTCTGGA						
	30 40 50 60 70 80						

	150	160	170	180	190	200	210
Hum.	GTTGAGGCTGGTCAATGGAGACGGTCCCTGCTCTGGACAGTGGAGGTGAAATTCACGGGACAGTGGGGG						
	: : : : :	: : : : :	: : : :	: : : :	: : : : :	: : : : :	: : : : :
WC1	GCTGAGGTTGAAGGATGGAGTCCATCGCTGTGAGGGGAGAGTGGAAGTGAAGCACCAAGGAGAAATGGGGC						
	90	100	110	120	130	140	150

	220	230	240	250	260	270
Hum.	ACTGTGTGATGATGGGTGAACACTACTGCCT-CAACTGTCGTGTGCAACACAGCTTGGATGTCATT					
 : : ..	:
WC1	ACAGTGGATGGTTACAGGTGA-CATTGAAGGATGCATCTGTAGTGTGCAGACAGCTGGGGTGTGGAGCT					
	160	170	180	190	200	210

Fig. 2Qi

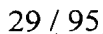
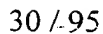


Fig. 2Qii



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Hum.  ACTTGAATACTGCTGCCGTGGTGTGCAGGCAACTAGGATGTCATCTTCTTTATTCTTCTGGAGTTGT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TCACACTTGCCCACTGCC-----CAG-----ATCATCTGT-----GCAGAGTTGGG
      490          500          510          520

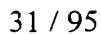
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	630	640	650	660	670	680	690
Hum.	TAATAGCCCTGCTGTATTGCGCCCCATTGGCTGGATGACATTTATGCCAGGGAATGAGTTGGCACT-						
	:...:::		:...:::	:...:::	:...:::	:...:::	:...:::
WC1	TTGTGGC-----AAGCTG--TGCTGT-----CCTGGGACATGAG---CTCTTT						
	530	540	550	560			

	700	710	720	730	740	750	760
Hum.	CTGGAATTGCAGACATCGTGGATGGGAAATCATGACTGCAGTCACAATGAGGATGTCACATTAACTTGT						
	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	:
WC1	CAGAGATCCAGT-GCC-----CAGGCTG-GGC---TGAAGAGTTCA-----GG						
	570	580	590	600			

	770	780	790	800	810	820	830
Hum.	TATGATAGTAGTATCTTGAAC	TAGGCTTGTAGGTGAAC	TAAACCGCTG	TATGGGAGAGTAGAGCTGA			
	:::::	:::	:::	:::	:::		:::
WC1	TGTGAGGGGAGGAGCCTGAGCT	-----CT-----	GGTCTGCCC-CAGAGTG-----	CCCTG-----			
	610	620	630	640	650		

Fig. 2Qiii



	840	850	860	870	880	890	900
Hum.	AAATCCAAGGAGTGGGGACCGTATGCCACCATAAGTGAACAATGCTGCAGCTGATGTCGTATGCAA						
	:::	::::	::::	::::	::::	::::	::::
WC1	---TCCA-----GGGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT						
		660	670	680	690	700	

	910	920	930	940	950	960	970
Hum.	GCAGTTGGGATGTGGAACCGCACTTCACTTCGCTGGCTTGCCTCATTTGCAGTCAGGCTGATGTTGTA						

WC1	ACT-----CAGAAAGTCGGCTCATGACAA-AC-GGCT--CCTC-TCAG-TGTGAAGGCAGGTGGAGAT						
	710	720	730	740	750	760	

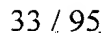
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Hum.   TGGCTTGATGTTCTCCTGCTCCGGTAATGAATCTTTTCTTTGGACTGCAGACATTCCGGAACCGTCA
      .:. .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
WC1    GAACATT-----TCTG-GACAATGGAGAGCGCTCTGTGCCCTCCC-CTGGAGTCTGGCCAATGCC---A
      770       780     790     800     810     820

```

[illegible]

Fig. 2Qiv



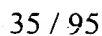
	1400	1410	1420	1430	1440	1450	1460
Hum.	CTGGAGTAATTGTTCTGATAAGGCAGATCTGGACCTAAGGCTTGTCGGGCTCATAGCCCCCTGTTATGG						
	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::
WC1	CTCAGA-----CAG--CAGGCAGCTCCG--CCTGGTG---GACGGGG-GC--GGTCCCTGCGCCGG						
1110		1120	1130		1140	1150	1160

	1470	1480	1490	1500	1510	1520
Hum.	GAGATTGGAGGTGAAATACCAAGGAGAGTGGGGACTGTGTCTATGACAGATGGAGCACAAGG-AAATGC					
	:::: ::::::: . . ::::::: ::::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
WC1	GAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGTATGACGGCTGGGAC-CTGGACGATGC					
	1170	1180	1190	1200	1210	1220

1530 1540 1550 1560 1570 1580 1590
Hum. A-GCTGTTGTGTAACAATTGGATGTGGA-AAGCCTATGCATGTGTTGGTATGACCTATTTAAAG
:: :: ::::: ::::: ::::: ::::: . . :: :: :: :::
WC1 CCGC-GTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCA-ATGCCACGGGGTCTGCTCACTTCGGGG
1230 1240 1250 1260 1270 1280 1290

	1600	1610	1620	1630	1640	1650	1660
Hum.	AAGCATCAGGACCTATTGGCTGGATGACGTTTCTTCATTGGAAATGAGTCAAATATCTGGACTGTGA						
	:: ::::::::::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
WC1	CAGGATCAGGGCCCATCTGGTTGGACAAC TTGA ACTGCACAGGAAAGAGTCCCACGTGTGGAGGTGCC						
	1300	1310	1320	1330	1340	1350	1360

Fig. 2Qvi



	1950	1960	1970	1980	1990	2000	2010
Hum.	ATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCATGCAGGAACAGTGGTG--GGGAAATAATGAC						

WC1	-AGAAATCCAGTGTGGGAAACTGACACCTCTCT---CTGGCAGTGTCTTCTGACCCCTTGGAATTACAAC						
	1640	1650	1660	1670	1680	1690	1700

	2020	2030	2040	2050	2060	2070	2080
Hum.	TGCAGTCACAGTGAAGATGTTGGAGTG-ATCTGTCTCATG-CATCGGATATGGAGCTGAGGCTTGTGGG						
	: :	: : :	: : :	: : :	: : :	: : :	: : :
WC1	T-CATGCTCTCCAAAGGAGGAAGCCTATATCTGGTGTGCAGACAGCACACA--GATCCGC--CTGGTGGA						
	1710	1720	1730	1740	1750	1760	

	2090	2100	2110	2120	2130	2140	2150
Hum.	TGGAAGCAGCAGGTGCTGTGAAAGTTGAGGTGAATGCCAGGGTGCCGTGGGAATCTGTGTGCTAAT						
	::::: . . : :	:::::	:::::	:::::	:::::	:::::	:::::
WC1	TGGAGGTGGTCGCTGCTCTGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGAC						
	1770	1780	1790	1800	1810	1820	1830

	2160	2170	2180	2190	2200	2210	2220
Hum.	GGCTGGGAATGAACATTGCTGAAGTTGTTTCAGGCAACTGAATGTGGTCTGCAATCAGGGTCTCCA						
	::::::::: ::::::::::: :::: :: ::::::::::: :: ::::::::::: :::: :: ::::: ::::						
WC1	CGCTGGGACCTGGACGATGCCCGTGTGTGTGTCACAGCAGCTGGGCTGTGGAGAAGC---CCTGGACGCCA						
	1840	1850	1860	1870	1880	1890	1900

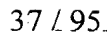
Fig. 2Qviii



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Hum. GAGA-GCCTCATTTACAGAA--AGAACATTACACATCTTAATGTCGAATCTGGCTGCACTGGAGGGGA
2230 2240 2250 2260 2270 2280
WC1 CTGTCTCTTCTTTCGGACGGGATCAGGCCCATCTGGCTGGATGAAGTGAAGTGCAGAGGAGAGGA
1910 1920 1930 1940 1950 1960 1970
2290 2300 2310 2320 2330 2340 2350
Hum. AGCCTCTCTCTGGGATTGTATACGATGGGAGTGGAAACAG-ACTGCGTGTCAATTAATATGGAAGCAAG
WC1 GTCCCAAGTATGGAGGTGCCCTTCCCTGGGGATGGCGGCAACACAAC-TGCAATCATCAAGAAGATGCAGG
1980 1990 2000 2010 2020 2030 2040
2360 2370 2380 2390 2400 2410 2420
Hum. TTTGATCTGCTCAGCCACAGGCAGCCAGGCTGGTTGGAGCTGATATGCCCTGCTCTGGACGTGTTGAA
WC1 AGTCATCTGCTCAGGATTTGTGC-----GTCTGGCTGGAGGAGATGGACCCCTGCTCAGGGCGAGTAGAA
2050 2060 2070 2080 2090 2100
2430 2440 2450 2460 2470 2480 2490
Hum. GTGAAACATGCAGACACATGGCGCTCTGTCTGTGATTCTGATTTCTCTCTTCATGCTGCCAATGT--GCT
WC1 GTGCATTCTGGAGAAGCCTGGACCCCAAGTGTCTGATGGAAACTTCACACTCCCACTGCCCAAGGTCATCT
2110 2120 2130 2140 2150 2160 2170

Fig. 2Qix



	2500	2510	2520	2530	2540	2550	2560
Hum.	GTGCAGAGAA	TAAATTGTGCAGATGCCATATCTCTTCTGTGGAGATC	ACTTGGAAAAGGG	-AATGG			
	:
WC1	GTGCAGAGC	--TGGGATGTGGCAAGGCTGTGTCT-GTCCTGGGACACATGCCATT	CAGAGAGTCCGATGG				
2180	2190	2200	2210	2220	2230	2240	

	2570	2580	2590	2600	2610	2620	2630
Hum.	TCTAACTTGGGCCCGAAAGTCCAGTGTGAAGGAGTGAAACTCACCTTGCCATTATGCCCCATTGTTCAA						

WC1	CCAGGTCTGGGCTGAAGAGTTCAGGTGTGATGGGGGGGAGCCTGAGCTCTGTGCTCTGCCCCAGAGTGCCC						
	2250	2260	2270	2280	2290	2300	2310

	2640	2650	2660	2670	2680	2690	2700
Hum.	CATCCGAAGACACTGTATCCACAGCAGAGAAGTTGGAGTTGCTCTGTTCCCGATATACAGATGTCCGAC						

WC1	TGTCCAGGAGGCACATGTCCTCCACAGTGGAGCTGCTCAGGTTGCTGTTCAGTGTACACAGAAGTCCAGC						
	2320	2330	2340	2350	2360	2370	2380

	2710	2720	2730	2740	2750	2760	2770
Hum.	TTGTGAATGGCAAAATCC---	CAGTGTGACGGGCAAGTGAGATCAACGTGCT-TGGACACTGGGGCTCAC					
	:::::..... ::	:::::..... :::::	:::::..... ::	:::::..... :::::	:::::..... :::::	:::::..... :::::	:::::..... :::::
WC1	TTATGAAAAACGGCACCCTCTCAATGTGAGGGGCAGGTGGAGAT-GAAGATCTCTGGACGATGGAGAGCGC						
	2390	2400	2410	2420	2430	2440	2450

Fig. 2Qx

Hum.	2780	2790	2800	2810	2820	2830	2840
	TGTGTGACACCCACTGGGACCCAGAAAGATGCCCGTGTTCATGCAGACAGCTCAGCTGTGGGACTGCTCT						
WC1	2460	2470	2480	2490	2500	2510	2520
	TCTGTGCCCTCCACTGGAGTCTGGCCAATGCCAATGTTGTCTGTCTCAGCTCGGCTGTGGAGTCGCCAT						
Hum.	2850	2860	2870	2880	2890	2900	2910
	CTCAACCACAGGAGGAAATATATTGGAGAAAGAGTGTTCGTGTGTGGGACACAGGTTTCATTGCTTA						
WC1	2530	2540	2550	2560	2570	2580	2590
	CTCCACCCAGAGGACCACTTGGTGAAGGAGGTGATCAGATCTCAACAGCCCCAATTTCACTGCTCA						
Hum.	2920	2930	2940	2950	2960	2970	2980
	GGGAATGAGTCACTTCTGGATAACTGTCAATGACAGTTCCTGGAGCACCTCCCTGTATCCATGGAAATA						
WC1	2600	2610	2620	2630	2640	2650	2660
	GGGGCTGAGTCCTTCCTGTGGAGTTGTCCTGTGACTGCCCTTGGGTGGGCTGACTGTTCCCATGGCAACA						
Hum.	2990	3000	3010	3020	3030	3040	3050
	CTGTCTCTGTGATCTGCACAGGAAGCCCTGACCCAGCCACTGTTTCCATGCCCTCGCAAATGTATCTGACCC						
WC1	2670	2680	2690	2700	2710	2720	2730
	CAGCCTCTGTGATCTCAGGAAACCAACCCAGGTGCTGCCCCAGTGCAACGACTTCTCTCAACC						

Fig. 2Qxi



Hum. ATATTGCTGCAGTTCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGAT
3060 3070 3080 3090 3100 3110 3120
WC1 TGCAGGCTCTCGGCCCTCAGAGGAGAGTTCTCCCTACTGCTCAGACAGCAGGCAGCTCCGCCTGGTGGAC
2740 2750 2760 2770 2780 2790 2800

Hum. GGGACAGCCGCTGTGCCGGGAGAGTAGAGATCTATCACGACGGCTTCTGGGGCACCATCTGTGATGACG
3130 3140 3150 3160 3170 3180 3190
WC1 GGGGGCGGTCCCTGCGGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGATG
2810 2820 2830 2840 2850 2860 2870

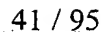
Hum. GCTGGACCTGAGCGATGCCACCGTGGTGTGTCAAAAGCTGGGCTGTGGAGTGGCCTTCAATGCCACGGT
3200 3210 3220 3230 3240 3250 3260
WC1 ACTGGGACCTGGACGATGCCCGTGTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCAATGCCACGGG
2880 2890 2900 2910 2920 2930 2940

Hum. CTCGTCTCACTTTGGGGAGGGGTCAAGGGCCCATCTGGCTGGATGACCTGAACTGCACAGGAACGGAGTCC
3270 3280 3290 3300 3310 3320 3330
WC1 GTCGTCTCACTTCGGGGCAGGATCAGGGCCCATCTGGCTGGACGACCTGAACCTGCACAGGAAGAGTCC
2950 2960 2970 2980 2990 3000 3010

Fig. 2Qxii

	3340	3350	3360	3370	3380	3390	3400
Hum.	CACTTGCCAGTGCCCTTCCCGCGGCTGGGGCAGCACGACTGCAGGCACAAGGAGGACGAGGGGTCA						
	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::
WC1	CACGTGTGAGGTGCCCTTCCCGCGGCTGGGGCAGCACGACTGCAGACACAAAGGAGGACGCCGGGGTCA						
	3020	3030	3040	3050	3060	3070	3080
	3410	3420	3430	3440	3450	3460	3470
Hum.	TCTGCTCAGAAATTCACAGCCCTTGAGGCTCTACAGTGAACACTGAAACAGAGAGCTGTGCTGGGAGATTGGA						
	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::
WC1	TCTGCTCAGAGTTCCTGGCCCTCAGGAT---GGTGAG-CGAGGACCAGCAG-TGTGCTGGGTGGCTGGA						
	3090	3100	3110	3120	3130	3140	
	3480	3490	3500	3510	3520	3530	3540
Hum.	AGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGGAACATCACCCACAGCCATAGCAGGCATTGTG						
	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::
WC1	GGTTTCTACAACGGGACCTGGGGCAGTGTCTGCCGCAGCCCCCATGGAAGATATCACTGTGTCCGTGATC						
	3150	3160	3170	3180	3190	3200	3210
	3550	3560	3570	3580	3590	3600	
Hum.	TGCAGGCAGCTGGGCTGTGGGGAGAAATGGAGTTGTACGCCTCGCCCCCTTA--TCT-AAGACAGGCTCTG						
	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::
WC1	TGCAGACAGCTTGGATGTGGGGACAGTGGGA--AGTCT-CAACACCTCTGTGTGGTCTCAGGGAAGGTCTTA						
	3220	3230	3240	3250	3260	3270	3280

Fig. 2Qxiii



	3610	3620	3630	3640	3650	3660	3670
Hum.	GTTTCATGTGGTGGATGACATT	CAGTGTCCTAAACGCATAT	CTCCATATGGCAGTGCC	TGTCTGCC	CCCC		
	..	:
WC1	GACCCCGTGGTAGATT	TAATTCAGTGTCGGAAAAT	GGATACCTCTCTCTGGCAGT	GTCTCTGGCCC			
	3290	3300	3310	3320	3330	3340	3350

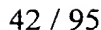
3680	3690	3700	3710	3720	3730	3740
Hum.	ATGGGAGCGAAGAA	TCCAGGCCAGCAG	AAGACCTGGATCA	CATGTGAAGATAGA	ATA---AGAG-	

WC1	ATGGAATACAGTCA	TGCTCTCCAAAGG	AGGAGCCTACATCT	CATGTGAAGGAAGA	AGACCCCAAGAGC	
3360	3370	3380	3390	3400	3410	3420

Hum.	-----TGC-----	3750	3760
	-----GTGGAGGACACCGAGTGCTCTG		
WC1	TGTCCAACTGCTGCCGCTGCACAGACAGAGAAGCTCCGCCTCAGGGGAGGACACAGCGAGTGCTCAG	:	:
	3430 3440 3450 3460 3470 3480 3490	:	:

	3770	3780	3790	3800	3810	3820	3830
Hum.	GGAGAGTGGAGATCTGGCACGCAGGCTCCTGGGCACAGTGTTGATGACTCCTGGGACCTGGCCGAGGC						
	:: :::::::::::	:::::::::::	:::::::::::	:::::::::::	:::::::::::	:::::::::::	:::::::::::
WC1	GGCGGGTGGAGGTGTGGCACACAACGGCTCCTGGGGCACCGTGTGCCGATGACTCCTGGAGCCTGGCAGAGGC						
	3500	3510	3520	3530	3540	3550	3560

Fig. 2Qxiv



3840	3850	3860	3870	3880	3890	3900
Hum.	GGA	GTGT	CAGCAGCTGGGCTGTGGCTCTGCTCTGGCTGCCCTGAGGGACGCTTCGTTGGCCAG			

WC1	TGAGGTGGTGT	CAGCAGCTGGGCTGTGGCCAGGCCCTGGAAGCCGTGCGGCTGCAGCATTTGGCCCT				
3570	3580	3590	3600	3610	3620	3630

[illegible]

	3980	3990	4000	4010	4020	4030	4040
Hum.	CCAAACCCTGGGACAGAGTGACTGTGGACACAAGGAAGATGCTGGCGTGAGGTGCTCTGG---	ACAGTC					
	:	:	:	:	:	:	:
WC1	CGGAGCCCCTGGGGGCAGAGCGACTGCAAGCACGAGGAGGATGCTGGTGTGAGGTGCTCTGGTGTAAAGC						
	3710	3720	3730	3740	3750	3760	3770

	4050	4060	4070	4080	4090
Hum. G-----CTGAATCACTGAATG--CCT-----CCTCAGGT-CATT---TAGCA-CTTATTTATCCA					
.					
WC1 AACATTGCCACGACCACAGCAGGACCAAGAACCTCAAATTCTCTCCCTGGCATCTTCTCCCTGCCT					
3780 3790 3800 3810 3820 3830 3840					

Fig. 2Qxv

Hum. G	4100	4110	4120	4130	4140
	-----TATCTT-----TGGGCTC-CTTCTC-----CTGGTTCT-----GTTTATCTATTCTCA				
:	:	:	:	:	:
WC1	3850	3860	3870	3880	3890
	GGGGTTCTCTGCCTTATCCTGGGGTCGCTTCTCTTCCCTGGTCCTCGTCATCCTGGTGACTCAGCTACTCA				
	3900	3910			
Hum.	4150	4160	4170	4180	
	CGTGGTG--CCGAGTTCAGAAACAAAACATCT-----GCCCT--CT--CAGAGTTT-----				
:	:	:	:	:	:
WC1	3920	3930	3940	3950	3960
	GATGGAGAGCAGAGCGCAGAGCCTTATCCAGCTATGAAGATGCTCTTGCTGAAGCTGTGTATGAGGAGCT				
	3970	3980			
Hum.	4190	4200	4210	4220	
	-----CAAC-----CAGAAGGAGGG---GTTCT-CTCG---AGGAGAAATTATTCCATGA-----				
:	:	:	:	:	:
WC1	3990	4000	4010	4020	4030
	CGATTACCTTCTGACACAGAAGGAAGTCTGGGCAGCCCAGATCAGATGATGTCCCTGATGAAAT				
	4040	4050			
Hum.	4230	4240	4250		
	---GATGGAG-----ACCTG-----CCTC-----AAGAGAGAGGAC				
:	:	:	:	:	:
WC1	4060	4070	4080	4090	4100
	TATGATGATGCTGAAGAAGTACCAGTGCCTGGAACTCCTTCTCCTCCTCAGGGGAATGAGGAGGAAGTGC				
	4110	4120			

Fig. 2Qxvi



```

4260      4270      4280      4290
Hum. CCACATGGGACAAGAAC-----CTCAGA-TGACAC---CC-----CCAA-----
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  CCCAGAGAAGGAGGACGGGTGAGGTCCTCTCAGACAGGCTCTTCTCCTGAAC TTCTCCAGAGAGGCAGC
4130      4140      4150      4160      4170      4180      4190
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Hum. -----CCATGGTT--GTGAAGA-----TGCTAGCGACAC-----ATCGCTG--TTGGGAGTT
      :: :: . :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  TAATCCTGGGGAAGGAGAGAAGAGAGCTTCTGGCTGCTCCAGGGGAAGAAAGGGGATGCTGGGTATGATGAT
4200      4210      4220      4230      4240      4250      4260
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Hum. CTT-----CCTG-----CCTCTGAAGCCACAAAA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  GTTGAAC TCAGTGCCTGGGGAACATCCCCCAGTGACTTTCTCG
4270      4280      4290      4300
      4310      4320      4330
      4340      4350
```

Fig. 2Qxvii



GTGACCCACGGTCCGGTCTGTGGCTGAGC ATG GCC A L P A L G L D P W S 12
L L G L F L F Q L L Q L L L P T T A G 67
CTC CTG GGC CTT TTC CTC CAA CTC CAG CTC CTG CTG CCG ACG ACC GCG GGG 32
G G G Q G P M P R V R Y Y A G D E R A 127
GGA GGC GGC CAG GGC CCC ATG CCC AGG GTC AGA TAC TAT GCA GGC GAT GAA CGT AGG GCA 52
L S F F H Q K G L Q D F D T L L L S G D 187
CTT AGC TTC TTC CAC CAG AAG GGC CTC CAG GAT TTT GAC ACT CTG CTC CTG AGT GGT GAT 72
G N T L L Y V G A R E A I L A L D I Q D P 247
GGA AAT ACT CTC TAC GTG GGC GCT CGA GAA GCC ATT CTG GCC TTG GAT ATC CAG GAT CCA 92
G V P R L K N M I P W P A S D R K K S E 307
GGG GTC CCC AGG CTA AAG AAC ATG ATA CCG TGG CCA GCC AGT GAC AGA AAA AAG AGT GAA 112
C A F K K K S N E T Q C F N F I R V L V 367
TGT GCC TTT AAG AAG AAG AGC AAT GAG ACA CAG TGT TTC AAC TTC ATC CGT GTC CTG GTT 132
S Y N V T H L Y T C G T F A F S P A C T 427
TCT TAC AAT GTC ACC CAT CTC TAC ACC TGC GGC ACC TTC GCC TTC AGC CCT GCT TGT ACC 152
F I E L Q D S Y L L P I S E D K V M E G 487
TTC ATT GAA CTT CAA GAT TCC TAC CTG TTG CCC ATC TCG GAG GAC AAG GTC ATG GAG GGA 172
547

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Fig. 3A



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K G Q S P F D P A H K H T A V L V D G M 192
AAA GGC CAA AGC CCC TTT GAC CCC GCT CAC AAG CAT ACG GCT GTC TTG GTG GAT GGG ATG 607

L Y S G T M N N F L G S E P I L M R T L 212
CTC TAT TCT GGT ACT ATG AAC TTC CTG GGC AGT GAG CCC ATC CTG ATG CGC ACA CTG 667

G S Q P V L K T D N F L R W L H H D A S 232
GGA TCC CAG CCT GTC CTC AAG ACC GAC AAC TTC CTC CGC TGG CTG CAT CAT GAC GCC TCC 727

F V A A I P S T Q V V Y F F F E E T A S 252
TTT GTG GCA GCC ATC CCT TCG ACC CAG GTC GTC TAC TTC TTC GAG GAG ACA GCC AGC 787

E F D F F E R L H T S R V A R V C K N D 272
GAG TTT GAC TTC TTT GAG AGG CTC CAC ACA TCG CGG GTG GCT AGA GTC TGC AAG AAT GAC 847

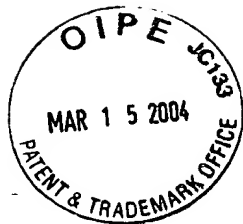
V G G E K L L Q K K W T T F L K A Q L L 292
GTG GGC GGC GAA AAG CTG CTG CAG AAG AAG TGG ACC ACC TTC CTG AAG GCC CAG CTG CTC 907

C T Q P G Q L P F N V I R H A V L L P A 312
TGC ACC CAG CCG GGG CAG CTG CTG CCC TTC AAC GTC ATC CGC CAC GCG GTC CTG CTC CCC GCC 967

D S P T A P H I Y A V F T S Q W Q V G G 332
GAT TCT CCC ACA GCT CCC CAC ATC TAC GCA GTC TTC ACC TCC CAG TGG CAG GTT GGC GGG 1027

T R S S A V C A F S L L D I E R V F K G 352
ACC AGG AGC TCT GCG GTT TGT GCC TTC TCT CTC TTG GAC ATT GAA CGT GTC TTT AAG GGG 1087

Fig. 3B



K Y K E L N K E T S R W T T Y R G P E T 372
AAA TAC AAA GAG TTG AAC AAA GAA ACT TCA CGC TGG ACT ACT TAT AGG GGC CCT GAG ACC 1147

N P R P G S C S V G P S S D K A L T F M 392
AAC CCC CGG CCA GGC AGT TGC TCA GTG GGC CCC TCC TCT GAT AAG GCC CTG ACC TTC ATG 1207

K D H F L M D E Q V V G T P L L V K S G 412
AAG GAC CAT TTC CTG ATG GAT GAG CAA GTG GTG GGC ACG CCC CTG CTG GTG AAA TCT GGC 1267

V E Y T R L A V E T A Q G L D G H S H L 432
GTG GAG TAT ACA CGG CTT GCA GTG GAG ACA GCC CAG GGC CTT GAT GGG CAC AGC CAT CTT 1327

V M Y L G T T T G S L H K A V V S G D S 452
GTC ATG TAC CTG GGA ACC ACC ACA GGG TCG CTC CAC AAG GCT GTG GTA AGT GGG GAC AGC 1387

S A H L V E E I Q L F P D P E P V R N L 472
AGT GCT CAT CTG GTG GAA GAG ATT CAG CTG TTC CCT GAC CCT GAA CCT GTT CGC AAC CTG 1447

Q L A P T Q G A V F V G F S G G V W R V 492
CAG CTG GCC CCC ACC CAG GGT GCA GTG TTT GTA GGC TTC TCA GGA GGT GTC TGG AGG GTG 1507

P R A N C S V Y E S C V D C V L A R D P 512
CCC CGA GCC AAC TGT AGT GTC TAT GAG AGC TGT GTG GAC TGT GTC CTT GCC CGG GAC CCC 1567

H C A W D P E S R T C C L L S A P N L N 532
CAC TGT GCC TGG GAC CCT GAG TCC CGA ACC TGT TGC CTC CTG TCT GCC AAC CTG AAC 1627

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Fig. 3C

S W K Q D M E R G N P E W A C A S G P M 552
TCC TGG AAG CAG GAC ATG GAG CCG GGG AAC CCA GAG TGG GCA TGT GCC AGT GGC CCC ATG 1687

S R S L R P P Q S R P Q I I K E V L A V P 572
AGC AGG AGC CTT CGG CCT CAG AGC CGC CCG CAA ATC ATT AAA GAA GTC CTG GCT GTC CCC 1747

N S I L E L P C P H L S A L A S Y Y W S 592
AAC TCC ATC CTG GAG CTC CCC TGC CCC CAC CTG TCA GCC TTG GCC TCT TAT TAT TGG AGT 1807

H G P A A V P E A S S T V Y N G S L L L 612
CAT GGC CCA GCA GTC CCA GAA GCC TCT TCC ACT GTC TAC AAT GGC TCC CTC TTG CTG 1867

I V Q D G V G G L Y Q C W A T E N G F S 632
ATA GTG CAG GAT GGA GTT GGG GGT CTC TAC CAG TGC TGG GCA ACT GAG AAT GGC TTT TCA 1927

Y P V I S Y W V D S Q Q D Q T L A L D P E 652
TAC CCT GTG ATC TCC TAC TGG GTG GAC AGC CAG GAC CAG ACC CTG GCC CTG GAT CCT GAA 1987

L A G I P R E H V K V P L T R V S G G A 672
CTG GCA GGC ATC CCC CGG GAG CAT GTG AAG GTC CCG TTG ACC AGG GTC AGT GGT GGG GCC 2047

A L A A Q Q S Y W P H F V T V T V L F A 692
GCC CTG GCT GCC CAG CAG TCC TAC TGG CCC CAC TTT GTC ACT GTC ACT GTC TTT GCC 2107

L V L S G A L I I L V A S P L R A L R A 712
TTA GTG CTT TCA GGA GCC CTC ATC ATC CTC GTG GCC TCC CCA TTG AGA GCA CTC CGG GCT 2167

Fig. 3D



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[illegible]

Fig. 3E



Hum.	10	20	30	40	50	60	70
	MALPALGLDPWSLLGLFLFQLLQLLP	TTAGGGQGPM	PRVRY	YAGDERRALS	FFHQKGLQ	DFDTLLS	
	
Mur.	10	20	30	40	50	60	70
	MALPSLGQDSWSLLRVFFQLFLLPSL	PPASGTGGQ	PMRVKY	HAGDGH	RALSFFQ	KGLRDFDTLLS	
	
Hum.	80	90	100	110	120	130	140
	GDGNTLYVGAREAILALDIQDPG	VPRLKNMIP	WPASDRK	KSECAFK	KKSNETQ	CNFIRVL	VSYNVTHLY
	
Mur.	80	90	100	110	120	130	140
	DDGNTLYVGARETVLALNIQNP	GIPLKNMIP	WPASERK	KTECAFK	KKSNETQ	CNFIRVL	VSYNATHLY
	
Hum.	150	160	170	180	190	200	210
	TCGTFAFSPACTFIELQDSYLL	PISEDKVME	GKGQSP	FDPAHKH	TAVLVDG	MLYSGTM	NFLGSEPILMR
	
Mur.	150	160	170	180	190	200	210
	ACGTFAFSPACTFIELQDSLL	LPILIDKVM	DGKGQSP	LTFTSTQ	AVLVDG	MLYSGTM	NFLGSEPILMR
	
Hum.	220	230	240	250	260	270	280
	TLGSQPVLKTDNFLRWLHHD	ASFVA	AIPTQV	YFFFEET	ASEDF	FFERLHT	SRVARVCKNDVGGEKLLQ
	
Mur.	220	230	240	250	260	270	280
	TLGSHPVLKTDIFLRLHAD	ASFVA	AIPTQV	YFFFEET	ASEDF	FEELYIS	RVAQVCKNDVGGEKLLQ
	

Fig. 3F

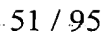


Fig. 3G



Hum. 570 580 590 600 610 620 630
RPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAPPEASSTVYNGSLLLIVQDGVGGLYQCWATENG
Mur. 560 570 580 590 600 610 620
PPQIIKEVLTVPNSILELPCPHLSALASYWSHGPAAPPEASSTVYNGSLLLIVQDGVGGLYQCWATENG
Hum. 640 650 660 670 680 690 700
FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTLFALVLSGALI
Mur. 630 640 650 660 670 680 690
YSYPVVSYWVDSQDQPLALDPELAGVPRERVQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIVLLGVLT
Hum. 710 720 730 740 750 760
ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDADNNCLGTEVA
Mur. 700 710 720 730 740 750 760
LLASPLGALRARGKVQCGGMLPPREKAPLSRDQHLQPSKDHRSTSASDADNNHLGAEVA

Fig. 3H

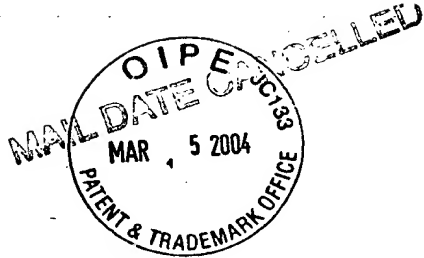
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Fig. 3I

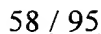


Fig. 3J

Hum.	530	540	550	560	570	580	590
	GGAGGACAAGGT	CATGGAGGAAAG	CCAAAGCCCTT	TGACCCCGCT	CACAAGCATACG	-GCTGTCTT	
Mur.	560	570	580	590	600	610	620
	GATAGACAAGGT	CATGGACGGGA	AGGGCCAAAGCCC	-TTTGACCCCT	GTTCACAAGCACACA	AGCTGTCTT	
Hum.	600	610	620	630	640	650	660
	GGTGGATGGGAT	GCTCTATTCTGG	TACTATGAACA	ACTTCCTGGC	CAGTGAGCCCCAT	CCTGATGCGCAC	
Mur.	630	640	650	660	670	680	690
	GGTCGATGGGAT	GCTTTATTCCGG	CCACCATGAACA	ACTTCCTGGC	CAGCGAGCCCCAT	CCTGATGCGGACA	
Hum.	670	680	690	700	710	720	730
	CTGGGATCCCAG	CCTGTCTCAAG	ACCGACAAC	TTCCTCCGCT	GGCTGCATCAT	GACGCCCTCCTTGTGG	
Mur.	700	710	720	730	740	750	760
	CTGGGATCCCAT	CCTGTCTCAAG	ACTGACATCTT	CTACGCTGG	CTGCACGCGGAT	GCCTCCTTCGTGG	
Hum.	740	750	760	770	780	790	800
	CAGCCATCCCCT	TCGACCCAGG	TCGTCTACTT	CTTCTTCGAG	GAGACAGCCAG	CGAGTTTGACTTCTTGA	
Mur.	770	780	790	800	810	820	830
	CAGCCATTCCAT	CCACCCAGG	TCGTCTATT	CTTCTTTGAG	GAGACAGCCAG	CGAGTTTGACTTCTTGA	

Fig. 3K

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	1370	1380	1390	1400	1410	1420	1430
Hum.	AGCGTGGTAAGTGGGACAGCAGTGC	TCATCTGGTGGAGAGATT	CAGCTGTTCCCTGACCC	TGAACC			
	::::::::::::	: ::::::::::::::	::::: ::::::::::::::	::::: ::::::::::::::	::::: ::::::::::::::	::::: ::::::::::::::	::::: ::::::::::::::
Mur.	AGGCTGGTGCCTCAGGACAGCAGTGC	TATCTCGTGGAGGAGATT	CAGCTGAGCCCTGACTCTGAGCC				
	1400	1410	1420	1430	1440	1450	1460

	1440	1450	1460	1470	1480	1490	1500
Hum.	TGTTCCGAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGCTGGAGG						

Mur.	TGTTCGAAACCTGCAGCTGGCCCCCGCCAGGGTGCAGTGTTCAGAGCTTCTCTGGAGGCATCTGGAGA						
	1470	1480	1490	1500	1510	1520	1530

	1510	1520	1530	1540	1550	1560	1570
Hum.	GTGCCCCAGCCAACTGATGTCTATGAGAGCTGTGGACTGTGCCTTGCCCGGACCCCCTGTTG						
	:: :: : :::::	:	: :::::	: :::::	: :::::	: :::::	: :::::
Mur.	GTTCCCAGGGCCAATTGCAGTGTCACGAGAGCTGTGTGGACTGTGTGCTTGCCAGGACCCTCACTGTG						
	1540	1550	1560	1570	1580	1590	1600

	1580	1590	1600	1610	1620	1630	1640
Hum.	CCTGGGACCC	TGAGTCCCGAAC	CTGTTCCTCCT	GCTGCTGCC	CCCCAACC	TGAAC	TCTTGAAGCAGGACAT
	:::::::::::::::	:: :::::	:::::::::	: : :::::	: : :::::	:	:::::::::::::::
Mur.	CCTGGGACCC	TGAATCAAGACT	CTGCAGCCTT	CTGTCTGGCTC	-TACCAAGCCT--	TGGAAGCAGGACAT	
	1610	1620	1630	1640	1650	1660	1670

Fig. 3N



Hum.	1650	1660	1670	1680	1690	1700	1710
	GGAGCGGGAA	CCAGAGTGG	CATGTGCC	AGTGGCCC	CATGAGC	AGGAGCCT	TGGCCCTCAGAGCCGC
	::::: ::	::::: ::	::::: ::	::::: ::	::::: ::	::::: ::	::::: ::
Mur.	GGAACGCGG	CAACCCG	AGTGGG	TATGCAC	CCCGTGG	CCCCCAT	GGCCAGGAGCCCCGGCGTCAGAGCCCC
	1680	1690	1700	1710	1720	1730	1740
Hum.	1720	1730	1740	1750	1760	1770	1780
	CCGCAAA	TCAATAA	AGATCCT	GGCTGT	CCCCAA	CTCCCA	CTCCCTGCGAGCTCCCTGCTCAG
	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::
Mur.	CCTCAAC	TAAATAA	AGATCCT	GACAGT	CCCCAA	CTCCAT	CCTGGAGCTGCGCTGCCCCACCTGTCAG
	1750	1760	1770	1780	1790	1800	1810
Hum.	1790	1800	1810	1820	1830	1840	1850
	CCTTGGC	CTCTTAT	TATGGAG	TATGGCC	CAGCAGC	AGTCCC	AGAGCCTCTTCCACTGTCTACAATGG
	:	::::: ::	:	:	:	:	:
Mur.	CAC	TGGCCTCT	TACCACT	GGAGT	CATGGCC	GAGCCAAA	ATCTCAGAAAGCCTCTGTACTACCGTCTACAATGG
	1820	1830	1840	1850	1860	1870	1880
Hum.	1860	1870	1880	1890	1900	1910	1920
	CTCCCTC	TGTGAT	AGTGCAG	GATGGAG	TGGGGT	CTCTACC	AGTGTGGGCAACTGAGAAATGGCTTT
	::::: ::	::::: ::	::::: ::	::::: ::	::::: ::	::::: ::	::::: ::
Mur.	CTCCCTC	TGTGCT	GCGCAG	GATGGT	GTGCGG	GCCTCT	ACCAGTGTGTGGCGACTGAGAACGGCTAC
	1890	1900	1910	1920	1930	1940	1950

Fig. 30

[illegible]

Fig. 3T

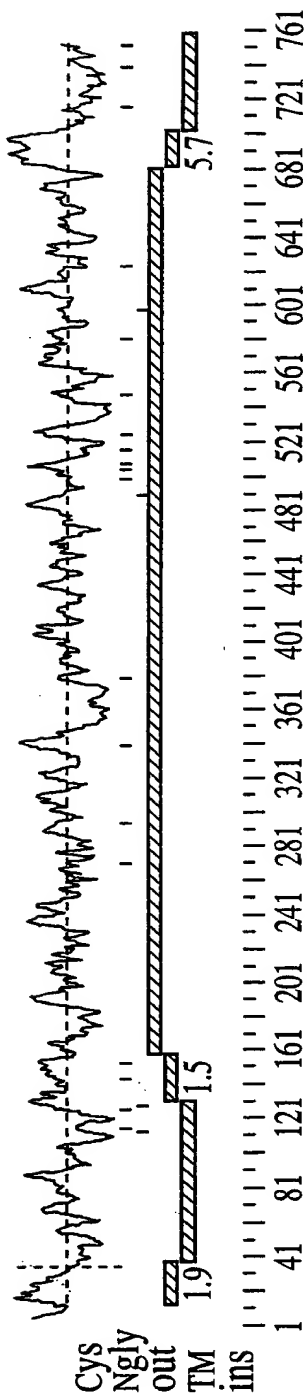


Fig. 3U



GTCGACCCACGGCTCCGGACGGCTGGGACGGCTCCCGGCTGCAGTCTGCCCGCCCGCGCGGGCCGAGTC

GC GAAGCGCGCTGC GACCCGGCTCCGGCGCGCTGGAGAGGACGCGAGAGCC ATG AGG CGC CAG CCT GCG 6
152

K V A A L L L G L L L E C T E A K K H C 26
AAG GTG GCG CTG CTG CTC GGG CTG CTC TTG GAG TGC ACA GAA GCC AAA AAG CAT TGC 212

W Y F E G L Y P T Y Y I C R S Y E D C C 46
TGG TAT TTC GAA GGA CTC TAT CCA ACC TAT TAT ATA TGC CGC TCC TAC GAG GAC TGC TGT 272

G S R C C V R A L S I Q R L W Y F W F L 66
GGC TCC AGG TGC TGT GTG CGG GCC CTC TCC ATA CAG AGG CTG TGG TAC TTC TGG TTC CTT 332

L M M G V L F C C G A G F F I R R R M Y 86
CTG ATG ATG GGC GTG CTT TTC TGC TGC GGA GCC GGC TTC TTC ATC CGG AGG CGC ATG TAC 392

P P P L I E E P A F N V S Y T R Q P P N 106
CCC CCG CCG CTG ATC GAG GAG CCA GCC TTC AAT GTG TCC TAC ACC AGG CAG CCC CCA AAT 452

P G P G A Q Q P G P P Y Y T D P G P G 126
CCC GGC CCA GGA GCC CAG CAG CCG GCG CCG CCC TAT TAC ACT GAC CCA GGA GGA CCG GGG 512

M N P V G N S M A M A F Q V P P N S P Q 146
ATG AAC CCT GTC GGC AAT TCC ATG GCA ATG GCT TTC CAG GTC CCA CCC AAC TCA CCC CAG 572

Fig. 4A



G S V A C P P P P A Y C N T P P P P Y E 166
GGG AGT GTG GCC TGC CCG CCC CCT CCA GCC TAC TGC AAC ACG CCT CCG CCC CCG TAC GAA 632

Q V V K A K * 173
CAG GTA GTG AAG GCC AAG TAG 653

TGGGGTGCCCAAGAGGAGACAGGAGGGCCCTTCCCTGGCCCTTCTGTCTTCGTTGATGTTCACTTCCAG 732
GAACGGTCTCGTGGCTGCTAAGGCGAGTCCCTCTGATATCCTCAGCAAGCACAGCTCTCTTCAGGCTTCCATGG 811
AGTACAAATATGAACTCACACTTGTCTCCTCTGTGCTTCTGTCTGACGCAGTCTGTCTCTCACATGGTAGTGT 890
GGTGACAGTCCCCGAGGGCTGACGTCCCTTACGGTGGCGTGACCCAGATCTACAGGAGAGAGACTGAGAGGAAGAGCAG 969
TGCTGGAGGTGCAGGTGGCATGTAGAGGGCCAGGCCGAGCATCCAGGCAAGCATCCTTCTGCCCCGGTATTAATAGG 1048
AAGCCCATGCGCGGCTCAGCCGATGAAGCAGCAGCCGACTGAGCTGAGCCAGCAGGTCTCTGCTCCAGCCTGT 1127
CCTCTCGTCAGCCTTCTCTCCAGAAAGCTGTTGGAGAGACATTCAGGAGAGAGCAAGCCCTTGTCTGTCTGTCT 1206
CTGTTTCATATCCTAAAGATAGACTTCTCTGCACCCGAGGAGGTAGCACGTGCAGCTCTCACCGCAGGATGGGGC 1285
CTAGAAATCAGGCTTGCCCTTGAGGCTTGACAGTGATCTGACATCCACTAAGCAAAATTTAATTCATGGGAAATCA 1364
CTTCTGCCCCAACTGAGACATTTGAGCTCTTGGTCTGATTTGGAGAAAGGACTGTTACCCATTTTGTG 1443
GTGTGTTTATGGAAGTGCATGTAGAGCGTCTGCCCCCTTGAATCAGACTGGGTGTGTCTTCCCTGGACATCACTGC 1522
CTCTCCAGGGCATTTCTAGGCCCCGGGGTCTCCTTCCCTCAGGCAGCTCCAGTGGTGGTCTGAAGGGTCTTCAA 1601
ACGGGGCACATCTGGCTGGGAAGTCACATGACTCTCCAGGGAGAGACCAAGCTGAGGCGTCTCTCTGAGGTTGT 1680
GTTGGGTCTAAGCGGGTGTGCTGGGCTCCAAGGAGGAGCTTGTGGGAAAGACAGGAGAACTGACTCAAC 1759
TGCACTGACCATGTTGTCAATAATAGAAATAAAGAAAGTGGTCGGAATGCACATTCCTGGATAGGAATCACAGCTCA 1838
CCCCAGGATCTCACAGGTAGTCTCCTGAGTAGTTGACGGCTAGCGGGAGCTAGTTCGCGGCATAGTTATAGTGTGA 1917
TGTGTGAACGCTGACCTGTCTGTGTCTAAGAGCTATGCAGCTTAGCTGAGGCGCCTAGATTACTAGATGTCTGTAT 1996
CACGGGGAATGAGGTGGGGTGCTTATTTTTTAATGAACATAATCAGAGCCTCTTGAGAAATTTGTACTCATTTGAAC 2075
AGCATCAAGACATCTCATGGAAGTGATACGGAGTGATTTGGTGTCCATGCTTTTCACTCTGAGGACATTTAATCGGAG 2154

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Fig. 4B



AACCTCCTGGGAATTTGTGGAGACACTTGGGAACAACAGACACCCCTGGGAATGCAGTTGCAAGCACAGATGCTG 2233
CCACCAGTGTCTGTGACACCCCTGGTGTGACTGCTGACTGCCAGCGGTGACCTCCCATGCTGCAGGCCCTCCATCTAAA 2312
TGAGACACAAGCACAAATGTTCACTGTTTACAAACCAAGACAACCTGCGTGGTCCAAACACTCCTCTTCTCCAGGTCA 2391
TTTGTGTTTGCAATTTTAAATGTCTTTTATTTTGTAAATGAAAAAGCACACTAAGCTGCCCCCTGGAATCGGGTGCAGCTGA 2470
ATAGGCACCCAAAAGTCCGTGACTAAATTTTCGTTTGTCTTTTGTATAGCAAAATATGTTAAGAGACAGTGTGGCTAGG 2549
GCTCAACAATTTGTATTTCCCATGTTTGTGTGAGACAGAGTTTGTGTTTCCCTTGAACCTGGTTAGAAATGTGCTACTGT 2628
GAACGCTGATCCTGCATATGGAAGTCCCACTTTGGTGACATTTCCCTGGCCATTTCTGTTTCCATTGTGTGGATGTTGGG 2707
TTGTGCCCCACTTCCCTGGAGTGAGACAGCTCCTGGTGTGTAATAATCCCGGAGCGTCCGTGGTTCAGAGTAAACTTGAAG 2786
CAGATCTGTGCATGCTTTTCCCTCTGCAACAATTTGGCTCGTTTCTCTTTTGTGTTCTTTTGTATAGGATCCCTGTTTCCT 2865
ATGTGTGCAAAATAAAAAATAAATTTGGGCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2944
AAAAAAAAGGGCGCCGC 2964

Fig. 4C

GTCGACCCACGCGTCCGGCCGCGGTCTTCTGCCGGCTTCAGCTCGTATCCCCGGAGTCCACCCGCCCGTCCCCGGGGT 79
GCGGACTGGCCCTGAGCTGGCCGTACAGCCCGGCTTCGGACGGTCTCGCTGGAGCC ATG GGC CGC CGG CTC 151
M G R R L 5
G R V A A L L L G L L V E C T E A K K H 25
GGC AGG GTG GCG CTG CTG CTC GGG CTG CTA GTG GAG TGC ACT GAG GCC AAA AAA CAT 211

Fig. 4D



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C W Y F E G L Y P T Y Y I C R S Y E D C 45
TGC TGG TAT TTT GAA GGA CTC TAT CCC ACA TAC TAT ATA TGC CGT TCC TAT GAA GAC TGC 271

C G S R C C V R A L S I Q R L W Y F W F 65
TGT GGC TCC AGG TGC TGT GTG AGG GCC CTT TCC ATA CAG AGG CTG TGG TAT TTT TGG TTC 331

L L M M G V L F C C G A G F I R R R M 85
CTG CTG ATG ATG GGT GTG CTG TTC TGC TGT GGT GCC GGT TTC ATT CGC CGG CGC ATG 391

Y P P P L I E E P T F N V S Y T R Q P P 105
TAT CCG CCA CCA CTC ATT GAG GAG CCC ACA TTC AAT GTG TCC TAT ACC AGG CAG CCA CCA 451

N P A P G A Q Q M G P P Y Y T D P G G P 125
AAT CCT GCT CCA GGA GCA CAG CAA ATG GGA CCG CCA TAT TAC ACC GAC CCT GGA GGA CCC 511

G M N P V G N T M A M A F Q V Q P N S P 145
GGG ATG AAT CCT GTT GGC AAT ACC ATG GCT ATG GCT TTC CAG GTC CAG CCC AAT TCA CCT 571

H G G T T Y P P P S Y C N T P P P Y 165
CAC GGA GGC ACA ACT TAC CCA CCC CCT TCC TAC TGC AAC ACG CCT CCA CCC CCC TAT 631

E Q V V K D K * 173
GAA CAG GTG AAG GAC AAG TAG 655

CAAGATGCTACATCAAAGGCAAGAGGATGGACAGGCCCTTTTGTACCTTCCCATCCTCACCAGATCTTGCTGATAG 734

Fig. 4E

GGTGGTCCAAAGGAAACTTGGATAATTCTCAAAGCAAGCCAGCTCTCTTTCAAGTCTTTTGTGGAGGACATTGGAATC 813
CACACTGTCTCCTCTGTTGCTTCTGTTCTGATGTAGTCTGTGCTCTCTGAGAGAGTGTGGCAACAGTCCCTGAGGGTT 892
GATATTCCTAGGGTGTCCAGGTAGATCCTCGGGAGAGAGGCTAAGGGAAAGGAAGGCATAGCCCTGTGTGTAGGGGG 971
CAGATAAAGTGTGAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACCTTCCGAAGAGACACTATCCACCA 1050
TCCAGCCCCATTCTCCTAATAGAAAGCTGTGGGGCTGTGTTGTTGATGCTCTTTGGTCTCCACTCACATTTTGAAAATAG 1129
GCTTTCCTCTGCAGGAATAGGAAAGACCCAAAGTACATAATTGCTTCCACTTAAATAAGAGGTGAGAACAGGCCCTCAG 1208
TTGGACATCTATAGTTAAATAAAGGCCATTAGAGAGGGGAAATCTTTAAGTTAGGGGAAATCTCTAAATGGAGACATT 1287
GCGTTTTATGAATCATCGTCTGGCTTTTCTTTTAGTGCATGTATTGAAGTGAGGTGTCCCTTTGAGATCAGATGGGGAG 1366
AGTGAACCTCTGCGGGGGTGGGTGTCTCTACTCAGAGGGCTCCAAACCCCTTTTCTTAGGTAGTTCTGTTGATGGGTT 1445
TTATGGGCACTATAGAGCTGAGGGGCACATTAGGCCGGGTAGTTACATTGACCCCTTGAGAGGAAGAGGACAGCCAAAG 1524
AAACTCAGCAAAAGCAAGACCAGCATTTGCTGAGTTAGAGCTAGGGTTGTATGTGATCCCAACAGAGATGTGCTGGCCCTCA 1603
GAAGAGGGGACGTTTGTGGATAGAGCCGTGAAAACCTACTTAGTTGCACAGATGACATAATCAAAAGTAGAGAAAGAAG 1682
TGAGTTAGAGATGCCATTTCCAGGTGAGAAATCAGAGCTCATCAGATAGATTACAAAGTAGTGGCTGGAGTTAACAGTA 1761
TGGAGTTCTTTTCCCTTGCGTAGTTAGTCACGTTGATGTGATTTAAACCCAGGTTGAGACCTTGTGTACTAAAGAGCAA 1840
GGAAGTATAGCTAAGATGTCTAGATTATTTATATGTAGTATGGTGGGAGTGGGCTGCAAGGAAGGGGCTGACATTG 1919
TAAATGAGAAATCAGAGCCATTGATAAACTGTACTTGTGATCAGGCATCCAAAGTGTCTCTTGAGTGGACATT 1998
GAGTATTTCTTACCACCTACAGACCAGGAGGCATGGTGTCAATTTCCATTGGGGTATTTATATGAGGTAGAGGTTTCCAG 2077
GAATCGACAGTAGCTGTGGGCTTAGTTTAAGGACTGAAAGCATAGGACTGGTAGACAGTTTCATAGGAAACTGCCG 2156
GGAAGGAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCATCATTTGAGCACCCCTTGTGTCTTGGC 2235
TTCCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGTCCCTTGTATACATAAGACAAAGCAACAATGTCTGTGTT 2314
TACAAATCAAGACGACTACATGGTCCAAACATTTCTTCTCTCTATCAGTTGTGGCTTTAACTTCCATTTCCTCCGTT 2393
CCTTTTAAATCAAGAAGCACAGTCAGAGCTGCCCTGGGATTGCATCAGGGAACGGCTGATCAAGGCATTCAAGTGC 2472
CATGACTAAATCTTATCTTTTGTATAGCAAAATCCCTTTAAGAAACTGAACAATTGCTAAGGCTCAGCAATTTTATATC 2551
CAATGTCTGTGAAGGTAAATTTTGTGTTGCCATTGAGCCCCACATTGGGAATTCCTTCTGACGTCAACACTGACAAATGCCT 2630
ATGGAAATTGCACCTTCTGGGTATATGTCCCAGCATCCTTGTCTTATGTTTGGTGAGTAAGGCTCACCCCTTCCAGC 2709

Fig. 4F



AGCTCTACTTCTGTGTGCTGAGGTCCTGTAGAGCCGGGCTTGGCACACAGACATGAGGCAGACTTGTGCATGCTCTTTC 2788
TTGGCAACACTTGGCTCATAATTTCTTCTCTTTTGATAGAGTCCTGTTCCTATGTATTTAAATAATAAAGTG 2867
AATTAGTCAAAAAAAAAAAAAAAAAAAAAAGGGCGGCGCGC 2915

Fig. 4G

	10	20	30	40	50	60	70
Hum.	MRRQPAKVAALLLGLLLECTEAKKHCWYFEGLYPTYICRSYEDCCGSRCCVRALS	QRLWYFWFLMMG					
	:	:	:	:	:	:	:
Mur.	MGRRLGRVAALLLGLLVECTEAKKHCWYFEGLYPTYICRSYEDCCGSRCCVRALS	QRLWYFWFLMMG					
	10	20	30	40	50	60	70
Hum.	VLFCGAGFFIRRRMYPPPLIEEPAFNVSYTRQPPNPGGAQQPGPPYYTD	PGGPMNPGNSMAMAFQV					
	:	:	:	:	:	:	:
Mur.	VLFCGAGFFIRRRMYPPPLIEEPTFNVSYTRQPPNAPGAQQMGPPYYTD	PGGPMNPGNTMAMAFQV					
	80	90	100	110	120	130	140
Hum.	PPNSPQGSVACPPPPAYCNTPPPPYEQVVKAK						
	:	:	:	:	:	:	:
Mur.	QPNSPHGGTTPPPPSYCNTPPPPYEQVVKDK						
	150	160	170				

Fig. 4H

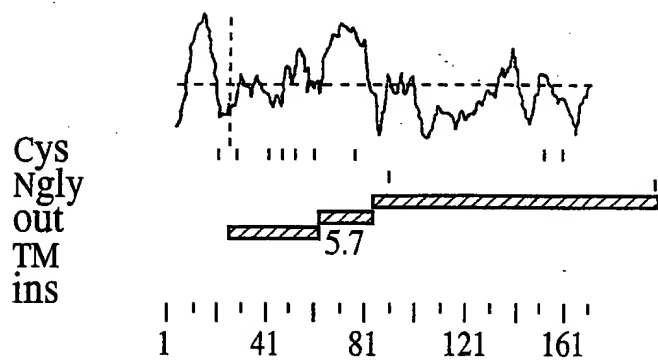


Fig. 4I

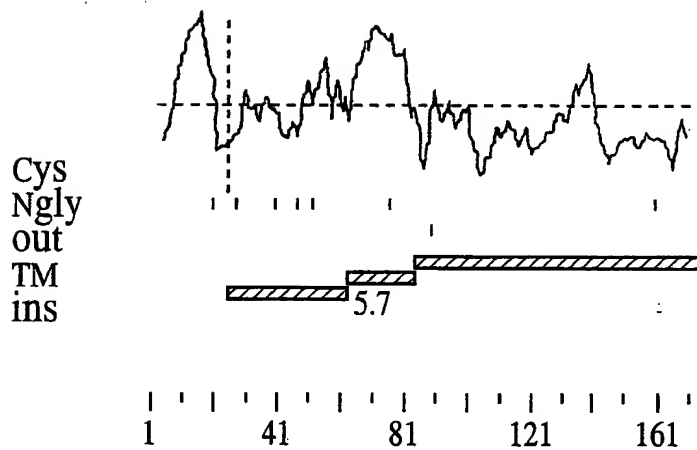


Fig. 4J

GTCGACCCACGGTCCGCAGCTTTGGACACTTCCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGGCAACTAAAGGA										79										
TCAAGAAAGGCCACAGCAGCAAGATCAGCTGGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC										150										
M C T K T I										6										
P	V	L	W	G	C	F	L	L	W	N	L	Y	V	S	S	S	Q	T	I	26
CCA	GTC	CTC	TGG	GGA	TGT	TTC	CTC	CTC	CTG	TGG	AAT	CTC	TAT	GTC	TCA	TCC	TCT	CAG	ACC	210
Y	P	G	I	K	A	R	I	T	Q	R	A	L	D	Y	G	V	Q	A	G	46
TAC	CCT	GGA	ATC	AAG	GCA	AGG	ATT	ACT	CAG	AGG	GCA	CTT	GAC	TAT	GGT	GTT	CAA	GCT	GGA	270
M	K	M	I	E	Q	M	L	K	E	K	K	L	P	D	L	S	G	S	E	66
ATG	AAG	ATG	ATT	GAG	CAA	ATG	CTA	AAA	GAA	AAG	AAA	CTC	CCA	GAT	TTA	AGC	GGT	TCT	GAG	330
S	L	E	F	L	K	V	D	Y	V	N	Y	N	F	S	N	I	K	I	S	86
TCT	CTT	GAA	TTT	CTA	AAA	GTT	GAT	TAT	GTA	AAC	TAC	AAT	TTT	TCA	AAT	ATA	AAA	ATC	AGT	390
A	F	S	F	P	N	T	S	L	A	F	V	P	G	V	G	I	K	A	L	106
GCC	TTT	TCA	TTT	CCA	AAT	ACC	TCA	TTG	GCT	TTT	GTG	CCT	GGA	GTG	GGA	ATC	AAA	GCG	CTA	450
T	N	H	G	T	A	N	I	S	T	D	W	G	F	E	S	P	L	F	V	126
ACC	AAC	CAT	GGC	ACT	GCC	AAC	ATC	AGC	ACA	GAC	TGG	GGG	TTC	GAG	TCT	CCA	CTT	TTT	GTT	510
L	Y	N	S	F	A	E	P	M	E	K	P	I	L	K	N	L	N	E	M	146
CTG	TAT	AAC	TCC	TTT	GCT	GAG	CCC	ATG	GAG	AAA	CCC	ATT	TTA	AAG	AAC	TTA	AAT	GAA	ATG	570

Fig. 5A



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L C P I I A S E V K A L N A N L S T L E	166
CTC TGT CCC ATT ATT GCA AGT GAA GTC AAA GCG CTA AAT GCC AAC CTC AGC ACA CTG GAG	630
V L T K I D N Y T L L D Y S L I S S P E	186
GTT TTA ACC AAG ATT GAC AAC TAC ACT CTG CTG GAT TAC TCC CTA ATC AGT TCT CCA GAA	690
I T E N Y L D L N L K G V F Y P L E N L	206
ATT ACT GAG AAC TAC CTT GAC CTG AAC TTG AAG GGT GTA TTC TAC CCA CTG GAA AAC CTC	750
T D P P F S P V P F V L P E R S N S M L	226
ACC GAC CCC CCC TTC TCA CCA GTT CCT TTT GTG CTC CCA GAA CGC AGC AAC TCC ATG CTC	810
Y I G I A E Y F F K S A S F A H F T A G	246
TAC ATT GGA ATC GCC GAG TAT TTC TTT AAA TCT GCG TCC TTT GCT CAT TTC ACA GCT GGG	870
V F N L T L S T E I S N H F V Q N S Q	266
GTT TTC AAT CTC ACT CTC TCC ACC GAA GAG ATT TCC AAC CAT TTT GTT CAA AAC TCT CAA	930
G L G N V L S R I A E I Y I L S Q P F M	286
GGC CTT GGC AAC GTG CTC TCC CGG ATT GCA GAG ATC TAC ATC TTG TCC CAG CCC TTC ATG	990
V R I M A T E P P I I N L Q P G N F T L	306
GTG AGG ATC ATG GCC ACA GAG CCT CCC ATA ATC AAT CTA CAA CCA GGC AAT TTC ACC CTG	1050
D I P A S I M M L T Q P K N S T V E T I	326
GAC ATC CCT GCC TCC ATC ATG ATG CTC ACC CAA CCC AAG AAC TCC ACA GTT GAA ACC ATC	1110

Fig. 5B

V S M D F V A S T S V G L V I L G Q R L 346
 GTT TCC ATG GAC TTC GTT GCT AGT ACC AGT GTT GGC CTG GTT ATT TTG GGA CAA AGA CTG 1170

 V C S L S L N R F R L A L P E S N R S N 366
 GTC TGC TCC TTG TCT CTG AAC AGA TTC CGC CTT GCT TTG CCA GAG TCC AAT CGC AGC AAC 1230

 I E V L R F E N I L S S I L H F G V L P 386
 ATT GAG GTC TTG AGG TTT GAA AAT ATT CTA TCG TCC ATT CTT CAC TTT GGA GTC CTC CCA 1290

 L A N A K L Q Q G F P L P N P H K F L F 406
 CTG GCC AAT GCA AAA TTG CAG CAA GGA TTT CCT CTG CCC AAT CCA CAC AAA TTC TTA TTC 1350

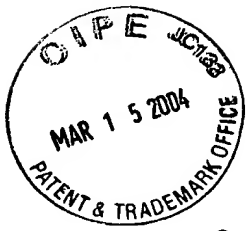
 V N S D I E V L E G F L L I S T D L K Y 426
 GTC AAT TCA GAT ATT GAA GTT CTT GAG GGT TTC CTT TTG ATT TCC ACC GAC CTG AAG TAT 1410

 E T S S K Q Q P S F H V W E G L N L I S 446
 GAA ACA TCC TCA AAG CAG CAG CCA AGT TTC CAC GTA TGG GAA GGT CTG AAC CTG ATA AGC 1470

 R Q W R G K S A P * 456
 AGA CAG TGG AGG GGG AAG TCA GCC CCT TGA 1500

 TTGCCGGTTTGAATTCACCCAGGAAGTAAATGGTCCTTAATCCTACAACTACTGTAAACCCAGAGGAAAGACAGT 1579
 ACACACTGGAATTGTAAAGCCCTTGTGAATTGCTTAGGCAGAAAGTTTCTTTCTTAAGCCTTCAGGAACCCAGAATAA 1658
 GGCAGACTCTGTAAAGGGATAAATAGAGGTGTCTGAATGTGAGTGTATGCATGCTGCGTGTCTGTGTTTATGTTG 1737
 TTTGTTTGTGGGCAAGAAAGATTCTAGGACAAGAGCTAGGCATGTACTTCTGACCAGGTGGTAAAGCAACTCTAAG 1816

Fig. 5C



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TCTGTATTGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTCCCCCTACCTGCATATTGGTTTC 1895
ATGTTTTATATTCACCTGTTACTATCTTCTGTGTTTAAATTGTTTCTATCAAAAAAAAAAAAAAAAAAGGGC 1974
GGCCGC 1980

Fig. 5D

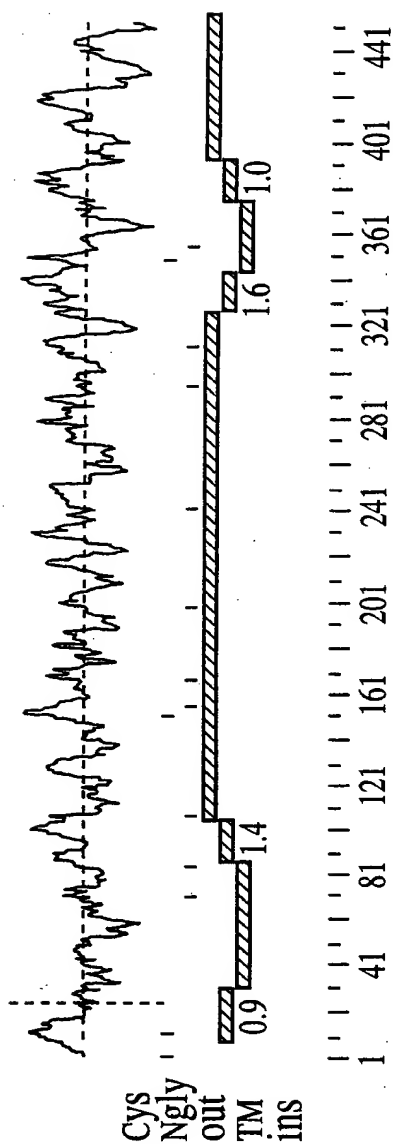


Fig. 5E

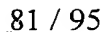


Fig. 51



GTCGACCCACGCGTCCGGGAATTGCAGCAGGAAATATGTGAAGAGTTTTTAAACCCACAAATCTTCTTACTTTAGA 79
ATTAGTTGTTACATTGGCAGGAAAAATAAATGCAGATGTTGGACC ATG TTG GAA ACC TTG TCA AGA CAG 149
M L E T L S R Q 8
W I V S H R M E M W L L I L V A Y M F Q 28
TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG 209
R N V N S V H M P T K A V D P E A F M N 48
AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT 269
I S E I I Q H Q G Y P C E E Y E V A T E 68
ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA 329
D G Y I L S V N R I P R G L V Q P K K T 88
GAT GGG TAT ATC CTT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA 389
G S R P V V L L Q H G L V G G A S N W I 108
GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT 449
S N L P N N S L G F I L A D A G F D V W 128
TCC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG 509
M G N S R G N A W S R K H K T L S I D Q 148
ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA 569

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Fig. 6A



D E F W A F S Y D E M A R F D L P A V I 168
GAT GAG TTC TGG GCT TTC AGT TAT GAT GAG ATG GCT AGG TTT GAC CTT CCT GCA GTG ATA 629

N F I L Q K T G Q E K I Y Y V G Y S Q G 188
AAC TTT ATT TTG CAG AAA ACG GGC CAG GAA AAG ATC TAT TAT GTC GGC TAT TCA CAG GGC 689

T T M G F I A F S T M P E L A Q K I K M 208
ACC ACC ATG GGC TTT ATT GCA TTT TCC ACC ATG CCA GAG CTG GCT CAG AAA ATC AAA ATG 749

Y F A L A P I A T V K H A K S P G T K F 228
TAT TTT GCT TTA GCA CCC ATA GCC ACT GTT AAG CAT GCA AAA AGC CCC GGC ACC AAA TTT 809

L L L P D M M I K G L F G K K E F L Y Q 248
TTG TTG CTG CCA GAT ATG ATG ATC AAG GGA TTG TTT GGC AAA AAA GAA TTT CTG TAT CAG 869

T R F L R Q L V I Y L C G Q V I L D Q I 268
ACC AGA TTT CTC AGA CAA CTT GTT ATT TAC CTT TGT GGC CAG GTG ATT CTT GAT CAG ATT 929

C S N I M L L L G G F N T N N M N M S R 288
TGT AGT AAT ATC ATG TTA CTT CTG GGT GGA TTC AAC ACC AAC AAT ATG AAC ATG AGC CGA 989

A S V Y A A H T L A G T S V Q N I L H W 308
GCA AGT GTA TAT GCT GCC CAC ACT CTT GCT GGA ACA TCT GTG CAA AAT ATT CTA CAC TGG 1049

S Q A V N S G E L R A F D W G S E T K N 328
AGC CAG GCA GTG AAT TCT GGT GAA CTC CGG GCA TTT GAC TGG GGC AGT GAG ACC AAA AAT 1109

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Fig. 6B



L E K C N Q P T P V R Y R V R D M T V P 348
CTG GAA AAA TGC AAT CAG CCA ACT CCT GTA AGG TAC AGA GTC AGA GAT ATG ACG GTC CCT 1169

T A M W T G G Q D W L S N P E D V K M L 368
ACA GCA ATG TGG ACA GGA GGT CAG GAC TGG CTT TCA AAT CCA GAA GAC GTG AAA ATG CTG 1229

L S E V T N L I Y H K N I P E W A H V D 388
CTC TCT GAG GTG ACC AAC CTC ATC TAC CAT AAG AAT ATT CCT GAA TGG GCT CAC GTG GAT 1289

F I W G L D A P H R M Y N E I I H L M Q 408
TTC ATC TGG GGT TTG GAT GCT CCT CAC CGT ATG TAC AAT GAA ATC ATC CAT CTG ATG CAG 1349

Q E E T N L S Q G R C E A V L * 424
CAG GAG GAG ACC AAC CTT TCC CAG GGA CGG TGT GAG GCC GTA TTG TGA 1397

AGCATCTGACACTGACGATCTTAGGACAACCTCCTGAGGGATGGGCTAGGACCCATGAAGGCAGAAATACGGAGAGCA 1476
GAGACCTAGTATACATTTTTCAGATTCCCTGCACCTTGGCACTAAATCCGACACTTACATTTTCTGTAAA 1555
TTAAAGTACTTATTAGGTAATAGAGGTTTGTATGCTATTATATATATCTTACCATCTTGAAGGGTAGGTTTACCTGAT 1634
AGCCAGAAAATATCTAGACATCTCTATATCATTCAGGTAATCTCTTAAACACCTATTGTTTTTCTATAAGCCAT 1713
ATTTTGGAGCACTAAAGTAAATGGCAAAATTTGGACAGATATTGAGGCTGGAGTCTGTGATTATTGTTGACTTTGA 1792
CAAAATAAGCTAGACATTTTCACCTTGTGCCCACAGACACATAACACTACCTCAGGAAGCTGAGCTGCTTTAAGGACAA 1871
CAACAACAAAATCAGTGTTACAGTATGGAATCTATGTTAAGCATTTCTCAGAATAAGGCCAAGTTTATAGTTGCA 1950
TCTCAGGGAAGAAAATTTTATAGGATGTTTATGAGTCTCCAATAAATGCATTCTGCATTACATAAAAAA 2029
AAAAAGGGGGCCGC 2044

Fig. 6C

```

      10    20    30    40    50    60    70
294 MLETLRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPTKAVDPEAFMNISEIIHQHGYPCPEEYEVATEDG
      :   . . . :   :   . . . :   :   :   :   :   :   :   :   :   :   :   :   :
HLPL M-----WLL---LTMASLISVLGTTHGLFGKLH----PGSPEVTMNISQMITYWGYPNEEYEVVTEGDG
      10    20    30    40    50

```

294	YILSVNRI	PRGLVQPKKTGSRPVLLQHGLVGASNWI	SNLPNNSLGFI	LADAGFDVW	MGNSRGN	AWSRK	
	:::	:::	:	:	:	:	:
	YILEVNR	IPYCKKNSGNTGQRPVFLQHGLLASATNWI	SNLPNNSLAFI	LADAGYDVW	LGNSRGNTW	ARR	
	60	70	80	90	100	110	120

	150	160	170	180	190	200	210
2294	HKTLSDQDEFWAFSYDEMAREFDLPAVINFILQKTGQEKIYVVGYSQGTTMGFIAFSTMPELAQAQIKIMYF						
	.	:	:	:	:	:	:
PHLP	NLYYSPDSVEFWAFSFDEMAKYDLPATIDFIVKKTGQQLHYVGHSGQTIGFIAFSTNPSLAKRIKTFY						
	130	140	150	160	170	180	190

	220	230	240	250	260	270
2294	ALAPIATVKHAKSPGTFELLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCGGVILDQICSNIMLLIGGF					
	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
2295	ALAPVATVKYTKSLINKLRFVPQSLEFKFIFGDKIF-YPHNFFDQLATEVCSEMLNLCSNALFIICGF					
	200	210	220	230	240	250
						260

Fig. 6D



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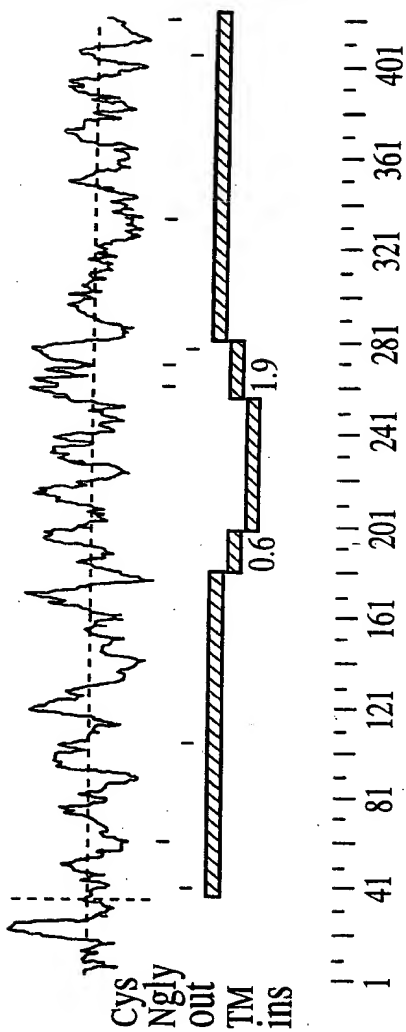


Fig. 6F

GTCGACCCACGCGTCCACGGCGAGGGCTCCCGGGCGCAGCATTTGCCCCCCTGCACCACCTCACCAAG ATG GCT 75

T L G H T F P F Y A G P K P T F P M D T 22
ACT TTG GGA CAC ACA TTC CCC TTC TAT GCT GGC CCC AAG CCA ACC TTC CCG ATG GAC ACC 135

T L A S I I M I F L T A L A T F I V I L 42
ACT TTG GCC AGC ATC ATC ATG ATC TTT CTG ACT GCA CTG GCC ACG TTC ATC GTC ATC CTG 195

P G I R G K T R L F W L L R V V T S L F 62
CCT GGC ATT CGG GGA AAG ACG AGG CTG TTC TGG CTG CTT CGG GTG GTG ACC AGC TTA TTC 255

I G A A I L A V N F S S E W S V G Q V S 82
ATC GGG GCT GCA ATC CTG GCT GTG AAT TTC AGT TCT GAG TGG TCT GTG GGC CAG GTC AGC 315

T N T S Y K A F S S E W I S A D I G L Q 102
ACC AAC ACA TCA TAC AAG GCC TTC AGT TCT GAG TGG ATC AGC GCT GAT ATT GGG CTG CAG 375

V G L G G V N I T L T G T P V Q Q L N E 122
GTC GGG CTG GGT GGA GTC AAC ATC ACA CTC ACA GGG ACC CCC GTG CAG CAG CTG AAT GAG 435

T I N Y N E E F T W R L G E N Y A E E C 142
ACC ATC AAT TAC AAC GAG GAG TTC ACC TGG CGC CTG GGT GAG AAC TAT GCT GAG GAG TGT 495

A K A L E K G L P D P V L Y L A E K F T 162
GCA AAG GCT CTG GAG AAG GGG CTG CCA GAC CCT GTG TTG TAC CTA GCT GAG AAG TTC ACT 555

Fig. 7A



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P R S P C G L Y R Q Y R L A G H Y T S A 182
CCA AGA AGC CCA TGT GGC CTA TAC CGC CAG TAC CGC CTG GCG GGA CAC TAC ACC TCA GCC 615

M L W V A F L L C W L L A N V M L S M P V 202
ATG CTA TGG GTG GCA TTC CTC TGC TGG CTG CTG GCC AAT GTG ATG CTC TCC ATG CCT GTG 675

L V Y G G Y M L L A T G I F Q L L A L L 222
CTG GTA TAT GGT GGC TAC ATG CTA TTG GCC ACC GGC ATC TTC CAG CTG TTG GCT CTG CTC 735

F F S M A T S L T S P C P L H L G A S V 242
TTC TTC TCC ATG GCC ACA TCA CTC ACC TCA CCC TGT CCC CTG CAC CTG GGC GCT TCT GTG 795

L H T H H G P A F W I T L T G L L C V 262
CTG CAT ACT CAC CAT GGG CCT GCC TTC TGG ATC ACA TTG ACC ACA GGA CTG CTG TGT GTG 855

L L G L A M A V A H R M Q P H R L K A F 282
CTG CTG GGC CTG GCT ATG GCG GTG GCC CAC AGG ATG CAG CCT CAC AGG CTG AAG GCT TTC 915

F N Q S V D E D P M L E W S P E E G L 302
TTC AAC CAG AGT GTG GAT GAA GAC CCC ATG CTG GAG TGG AGT CCT GAG GAA GGT GGA CTC 975

L S P R Y R S M A D S P K S Q D I P L S 322
CTG AGC CCC CGC TAC CGG TCC ATG GCT GAC AGT CCC AAG TCC CAG GAC ATT CCC CTG TCA 1035

E A S S T K A Y C K E A H P K D P D C A 342
GAG GCT TCC ACC AAG GCA TAC TGT AAG GAG GCA CAC CCC AAA GAT CCT GAT TGT GCT 1095

Fig. 7B

L	344	
*	1101	
TTA TAA		
CATTCTCCCCGTGGAGGCCACCTGGACTTCCAGTCTGGCTCCAAACCTCATTTGGCGCCCCATAAAACCAGCAGAACTG	1180	
CCCTCAGGGTGGCTGTTACAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAGGAGGCTCTATATACTGATGTT	1259	
AAAAACAAAACAAAAGCCCTAAGGACTGAAGAGATGCTGGGCTGTCCATAAAGCCTGTTGCCATGATAAG	1338	
GCCAAGCAGGGCTAGCTTATCTGCACAGCAACCCAGCCTTTCCGTGCTGCCCTTCCCTCTCAAGATGCTATTCACTGA	1417	
AACCTAACTTCACCCCCATAAACACAGCAGGGTGGGGTTACATAATGATTCTCCATATGGTTTCCCTCATCCCCTCGGCA	1496	
CCCTTGTTTTCCTTTTCCCTGGTTCCTTTTGTCTTACTTCTCCAGCTTGTGTGGCCTTTTGGTACAATGAA	1575	
AGACAGCACTGGAAAGGAGGGGAAACCAACTTCTCATCCTAGGTCTAACATTAAACCACTATGCCACATTCCTTTGA	1654	
GCTTCAGTTCCTCCAAATTTGCTACATAAGATTGCAAGACTTGCCAAGAATCTTGGGATTTATCTTCTATGCCCTTGCTGA	1733	
CACCTACCTTGGCCCTCAAAACACCACTCACAGAAGCCAGGTGGGAAGTAGGGAATCAACTCCAAAACGCTATTCTT	1812	
TCCACCCCACTCAGCTGGGCTAGCTGAGTGGCATCCAGGACGGGGAGTGGTGACCTGCCTCATCACTGCCACCTAA	1891	
CGTCCCCCTGGGTGTTCAGAAAAGATGCTAGCTCTGGTAGGTCCCTCCGGCCCTCACTAGAGGGCGCCCTATTACTC	1970	
TGGAGTCGACGCAGAGAAATCAGGTTTCACAGCACTGCGGAGAGTGTAAGGTGTCTCCAGCCCGAGCGAAGCTCATGA	2049	
GGACGTGCGACCCCGCGCGGAGAGCCATGAAAATTATGGGAAAAAACAGTTTTTAAAAAAGGGGCG	2128	
GCCGC	2133	

Fig. 7C

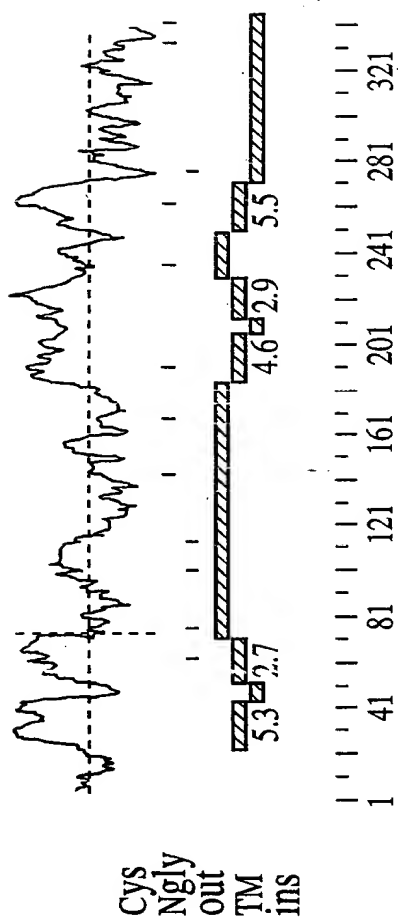


Fig. 7D

296	MATLGH	TFPFYAGPKPTFPMD	TTLASII	MIFLTALATFIVILPGIRGKTRFLWLLRVVTS	SLFIGAA	ILAV	10	20	30	40	50	60	70
:	:	:	:	:	:	:	:
CRP	M-RIAH	-----ASSRGNI	-----SIFSVFLIPLIAYILILPGVR	-RKR	VVT	TVTYVLM	LA	V	G	G	A	L	I
							10	20	30	40	50		
296	NFSSEWSVGQVSTNTSYKAFSSEWISADIGLQVGLGVNITL	-----TGTPVQQ	LN	ETIN	--YNEEFTW		80	90	100	110	120	130	
:	:	:	:	:	:	:	:
CRP	LIYPCWASGSQMIYTQFRGHSNERILAKIGVEIGLQKVNVT	LKFERLLSSNDVLP	GS	DMTELYYNEGF	DI		60	70	80	90	100	110	120
296	RLGENYAECAKALEKGLDPVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWVAF	LCWLLANV-MLSM					140	150	160	170	180	190	200
:	:	:	:	:	:	:	:
CRP	SGISSMAEALHHGLENGLPYPMLSVLEYFSLNQDSFDWGRHYRVAGHYTHAAIWFA	FCWCLSVVLMFL					130	140	150	160	170	180	190
296	PVLVYGGYMLLATGIFQLLALLFFSMATSLTSPCPLHL	---GASVLTHHGPAF	---WITLT	TGLLCVL			210	220	230	240	250	260	
:	:	:	:	:	:	:	:
CRP	PHNAYKS--ILATGISCLIA	CLVYL---LLSPCELRI	AFTGENFERVDLTATFS	CFYLIFAIGILCVL			200	210	220	230	240	250	260

Fig. 7E

